

STIC-Biotech/ChemLib

85118

From: Kallis, Russell
Sent: Friday, January 24, 2003 12:34 PM
To: STIC-Biotech/ChemLib
Subject: sequence search request

Hey there!

Sequence search request

Russ Kallis
79117
AU 1638
room 9D06
phone 305-5417
mail CM1 9 E12

case 09/807867

OLIGO search of SEQ ID NO: 1 vs the nucleotide database

SEQ ID NO: 2 vs the protein database

cheers,
Russ

CRF

Point of Contact:
Susan Hanley
Technical Info. Specialist
CM1 6B05 Tel: 305-4053

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

1

1

WEST[Help](#)[Logout](#)[Interrupt](#)[Main Menu](#)[Search Form](#)[Posting Counts](#)[Show S Numbers](#)[Edit S Numbers](#)[Preferences](#)[Cases](#)**Search Results -**

Terms	Documents
L6 and carotenoid.ab.	19

Database: US Patents Full-Text Database ▲
US Pre-Grant Publication Full-Text Database
JPO Abstracts Database
EPO Abstracts Database
Derwent World Patents Index
IBM Technical Disclosure Bulletins ▼

Search:

L7

[Refine Search](#)[Recall Text](#)[Clear](#)**Search History**DATE: Thursday, February 20, 2003 [Printable Copy](#) [Create Case](#)**Set Name Query**
side by side**Hit Count Set Name**
result set

DB=USPT,DWPI; PLUR=YES; OP=OR

<u>L7</u>	L6 and carotenoid.ab.	19	<u>L7</u>
<u>L6</u>	modification and carotenoid and biosynthesis and pathway	176	<u>L6</u>
<u>L5</u>	TOCB	1	<u>L5</u>
<u>L4</u>	TOCB and carotenoid	0	<u>L4</u>
<u>L3</u>	L2 and terminal and oxidase	1	<u>L3</u>
<u>L2</u>	L1 and carotenoid.ab.	55	<u>L2</u>
<u>L1</u>	carotenoid and biosynthesis and plant	296	<u>L1</u>

END OF SEARCH HISTORY

\$%^STN;HighlightOn= ***;HighlightOff=*** ;

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NEWS	3	Apr 09	BEILSTEIN: Reload and Implementation of a New Subject Area
NEWS	4	Apr 09	ZDB will be removed from STN
NEWS	5	Apr 19	US Patent Applications available in IFICDB, IFIPAT, and IFIUDB
NEWS	6	Apr 22	Records from IP.com available in CAPLUS, HCAPLUS, and ZCAPLUS
NEWS	7	Apr 22	BIOSIS Gene Names now available in TOXCENTER
NEWS	8	Apr 22	Federal Research in Progress (FEDRIP) now available
NEWS	9	Jun 03	New e-mail delivery for search results now available
NEWS	10	Jun 10	MEDLINE Reload
NEWS	11	Jun 10	PCTFULL has been reloaded
NEWS	12	Jul 02	FOREGE no longer contains STANDARDS file segment
NEWS	13	Jul 22	USAN to be reloaded July 28, 2002; saved answer sets no longer valid
NEWS	14	Jul 29	Enhanced polymer searching in REGISTRY
NEWS	15	Jul 30	NETFIRST to be removed from STN
NEWS	16	Aug 08	CANCERLIT reload
NEWS	17	Aug 08	PHARMAMarketLetter(PHARMAML) - new on STN
NEWS	18	Aug 08	NTIS has been reloaded and enhanced
NEWS	19	Aug 19	Aquatic Toxicity Information Retrieval (AQUIRE) now available on STN
NEWS	20	Aug 19	IFIPAT, IFICDB, and IFIUDB have been reloaded
NEWS	21	Aug 19	The MEDLINE file segment of TOXCENTER has been reloaded
NEWS	22	Aug 26	Sequence searching in REGISTRY enhanced
NEWS	23	Sep 03	JAPIO has been reloaded and enhanced
NEWS	24	Sep 16	Experimental properties added to the REGISTRY file
NEWS	25	Sep 16	CA Section Thesaurus available in CAPLUS and CA
NEWS	26	Oct 01	CASREACT Enriched with Reactions from 1907 to 1985
NEWS	27	Oct 21	EVENTLINE has been reloaded
NEWS	28	Oct 24	BEILSTEIN adds new search fields
NEWS	29	Oct 24	Nutraceuticals International (NUTRACEUT) now available on STN
NEWS	30	Oct 25	MEDLINE SDI run of October 8, 2002
NEWS	31	Nov 18	DKILIT has been renamed APOLLIT
NEWS	32	Nov 25	More calculated properties added to REGISTRY
NEWS	33	Dec 02	TIBKAT will be removed from STN
NEWS	34	Dec 04	CSA files on STN
NEWS	35	Dec 17	PCTFULL now covers WP/PCT Applications from 1978 to date
NEWS	36	Dec 17	TOXCENTER enhanced with additional content
NEWS	37	Dec 17	Adis Clinical Trials Insight now available on STN
NEWS	38	Dec 30	ISMEC no longer available

NEWS 39 Jan 13 Indexing added to some pre-1967 records in CA/CAPLUS
 NEWS 40 Jan 21 NUTRACEUT offering one free connect hour in February 2003
 NEWS 41 Jan 21 PHARMAML offering one free connect hour in February 2003
 NEWS 42 Jan 29 Simultaneous left and right truncation added to COMPENDEX,
 ENERGY, INSPEC
 NEWS 43 Feb 13 CANCERLIT is no longer being updated

NEWS EXPRESS January 6 CURRENT WINDOWS VERSION IS V6.01a,
 CURRENT MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP),
 AND CURRENT DISCOVER FILE IS DATED 01 OCTOBER 2002
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FULL ESTIMATED COST	0.21	0.21

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=> s TOCB and carotenoid

L1 0 TOCB AND CAROTENOID

=> s carotenoid(w)biosynthes? and rate(w)limiting

L2 8 CAROTENOID(W) BIOSYNTHES? AND RATE(W) LIMITING

=> duplicate remove l2

DUPLICATE PREFERENCE IS 'BIOSIS, EMBASE, CAPLUS'

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PROCESSING COMPLETED FOR L2

L3 4 DUPLICATE REMOVE L2 (4 DUPLICATES REMOVED)

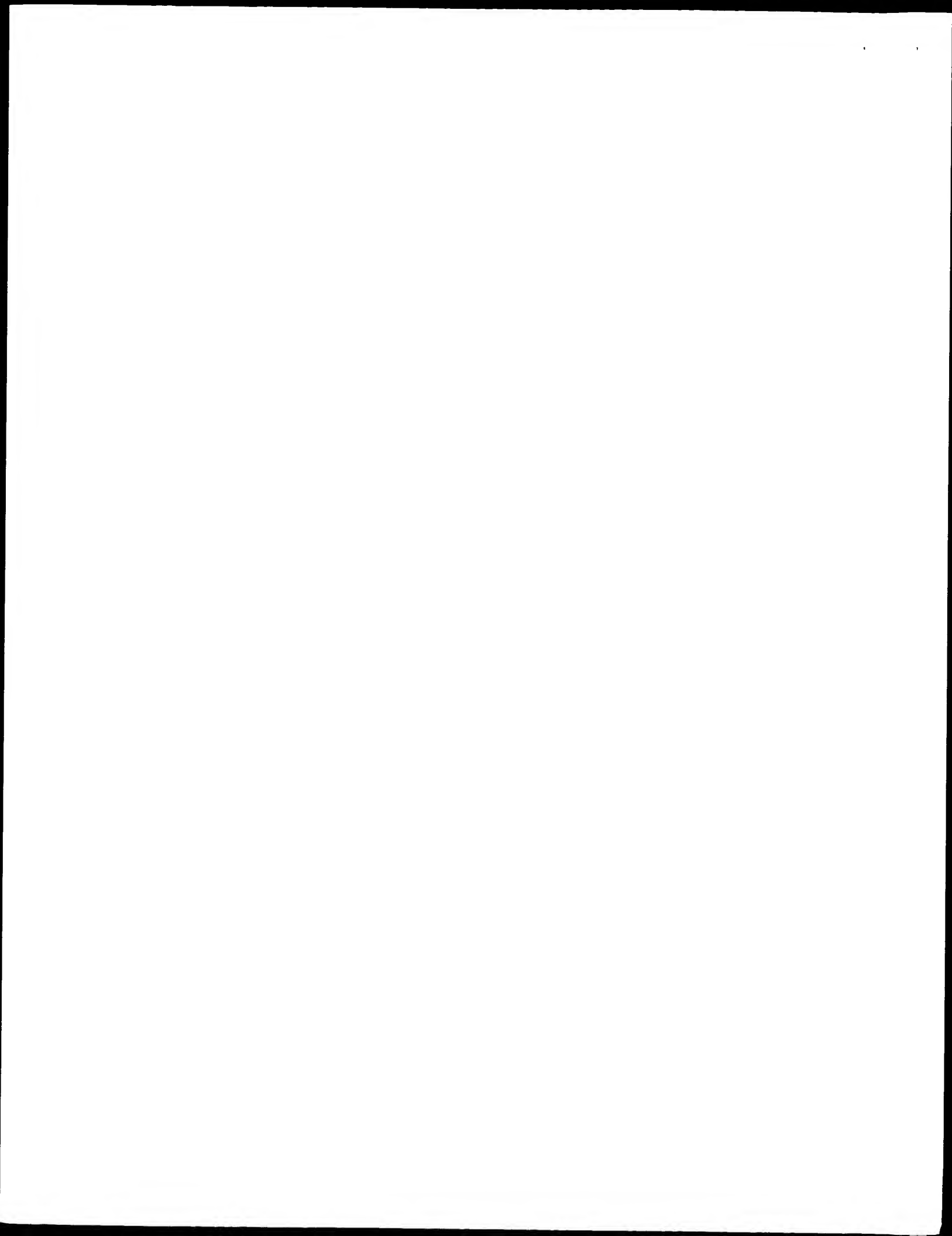
=> d 13 1-4

L3 ANSWER 1 OF 4 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
AN 94252943 EMBASE
DN 1994252943
TI Eubacteria show their true colors: Genetics of carotenoid pigment biosynthesis from microbes to plants.
AU Armstrong G.A.
CS Department of Plant Genetics, Institute for Plant Sciences, Swiss Federal Technology Institute, CH-8092 Zurich, Switzerland
SO Journal of Bacteriology, (1994) 176/16 (4795-4802).
ISSN: 0021-9193 CODEN: JOBAAY
CY United States
DT Journal; (Short Survey)
FS 004 Microbiology
LA English
SL English

L3 ANSWER 2 OF 4 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 1
AN 1993:432359 BIOSIS
DN PREV199396086984
TI Molecular and biochemical characterization of herbicide-resistant mutants of cyanobacteria reveals that phytoene desaturation is a ***rate*** -
limiting step in ***carotenoid*** ***biosynthesis*** .
AU Chamovitz, Daniel; Sandmann, Gerhard; Hirschberg, Joseph (1)
CS (1) Dep. Genetics, Hebrew Univ. Jerusalem, Jerusalem 91904 Israel
SO Journal of Biological Chemistry, (1993) Vol. 268, No. 23, pp. 17348-17353.
ISSN: 0021-9258.
DT Article
LA English

L3 ANSWER 3 OF 4 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 2
AN 1993:499191 BIOSIS
DN PREV199396123198
TI Molecular cloning and sequence analysis of the crtB gene of Thermus thermophilus HB27, an extreme thermophile producing carotenoid pigments.
AU Hoshino, Takayuki (1); Fujii, Ryouji; Nakahara, Tadaatsu
CS (1) Inst. Applied Biochem., Univ. Tsukuba, Tsukuba, Ibaraki 305 Japan
SO Applied and Environmental Microbiology, (1993) Vol. 59, No. 9, pp. 3150-3153.
ISSN: 0099-2240.
DT Article
LA English

L3 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2003 ACS
AN 1994:209642 CAPLUS
DN 120:209642
TI Functional expression of the Erwinia uredovora ***carotenoid***
biosynthesis gene crtI in transgenic plants showing an increase
of .beta.-carotene biosynthesis activity and resistance to the bleaching herbicide norflurazon
AU Misawa, Norihiko; Yamano, Shigeyuki; Linden, Hartmut; de Felipe, Maria R.; Lucas, Mercedes; Ikenaga, Hiroshi; Sandmann, Gerhard
CS Cent. Lab. Key Technol., Kirin Brew. Co., Ltd, Yokohama, 236, Japan



SO Plant Journal (1993), 4(5), 833-40
CODEN: PLJUED; ISSN: 0960-7412
DT Journal
LA English

=> FIL STNGUIDE

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ENTRY	SESSION
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ENTRY	SESSION
0.06	22.40

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=> s carotenoid(w)biosynthes? and plant(w)transform?

L4 7 CAROTENOID(W) BIOSYNTHES? AND PLANT(W) TRANSFORM?

=> duplicate remove l4

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PROCESSING COMPLETED FOR L4

L5 4 DUPLICATE REMOVE L4 (3 DUPLICATES REMOVED)

=> d l5 1-4

L5 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2003 ACS

AN 2002:963266 CAPLUS

TI Stimulation of carotenoid metabolism in arbuscular mycorrhizal roots

AU Fester, Thomas; Schmidt, Diana; Lohse, Swanhild; Walter, Michael H.;
Giuliano, Giovanni; Bramley, Peter M.; Fraser, Paul D.; Hause, Bettina;
Strack, Dieter

CS Leibniz-Institut fur Pflanzenbiochemie, Abteilung Sekundarstoffwechsel,
Halle/Saale, 06120, Germany

SO Planta (2002), 216(1), 148-154

CODEN: PLANAB; ISSN: 0032-0935
PB Springer-Verlag
DT Journal
LA English
RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 2 OF 4 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 1
AN 2001:37726 BIOSIS
DN PREV200100037726
TI The chloroplast and leaf developmental mutant, pale cress, exhibits light-conditional severity and symptoms characteristic of its ABA deficiency.
AU Holding, David R. (1); Springer, Patricia S.; Coomber, Shirley A.
CS (1) Department of Botany and Plant Sciences, University of California, Riverside, CA, 92521: dholding@ucr.ac1.ucr.edu USA
SO Annals of Botany (London), (November, 2000) Vol. 86, No. 5, pp. 953-962. print.
ISSN: 0305-7364.
DT Article
LA English
SL English

L5 ANSWER 3 OF 4 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 2
AN 2001:49727 BIOSIS
DN PREV200100049727
TI Identification of a novel gene coding for neoxanthin synthase from Solanum tuberosum.
AU Al-Babili, Salim; Hugueney, Philippe; Schledz, Michael; Welsch, Ralf; Frohnmeyer, Hanns; Laule, Oliver; Beyer, Peter (1)
CS (1) Center for Applied Biosciences, University of Freiburg, Schaeenzlestr. 1, D-79104, Freiburg: beyer@uni-freiburg.de Germany
SO FEBS Letters, (24 November, 2000) Vol. 485, No. 2-3, pp. 168-172. print.
ISSN: 0014-5793.
DT Article
LA English
SL English

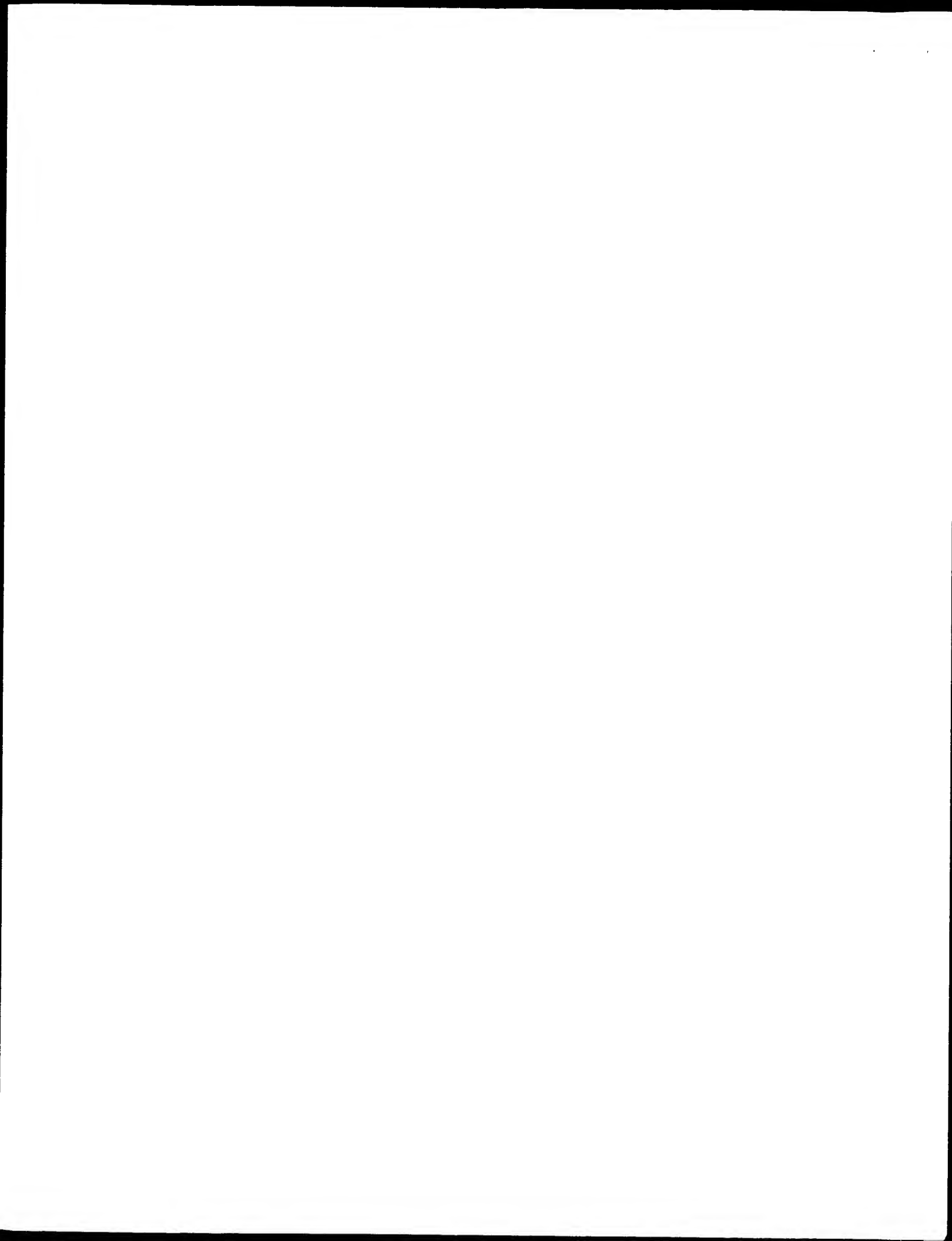
L5 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2003 ACS
AN 1995:999495 CAPLUS
DN 124:48378
TI Studies on ***carotenoid*** ***biosynthesis*** using the methods of natural products chemistry, molecular biology, and metabolic engineering
AU Misawa, Norihiko
CS Cent. Lab. Key Technol., Kirin Brew. Co., Ltd., Yokohama, 236, Japan
SO Nippon Nogei Kagaku Kaishi (1995), 69(12), 1567-72
CODEN: NNKKAA; ISSN: 0002-1407
DT Journal; General Review
LA Japanese

=> s carotenoid? and plant(w)transform?

L6 18 CAROTENOID? AND PLANT(W) TRANSFORM?

=> duplicate remove l6

DUPLICATE PREFERENCE IS 'AGRICOLA, BIOSIS, EMBASE, CAPLUS'



KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n

PROCESSING COMPLETED FOR L6

L7 9 DUPLICATE REMOVE L6 (9 DUPLICATES REMOVED)

=> d 17 1-9

L7 ANSWER 1 OF 9 CAPLUS COPYRIGHT 2003 ACS

AN 2002:123201 CAPLUS

DN 136:162385

TI Methyl-D-erythritol phosphate pathway gene gcpE from Arabidopsis thaliana and other plants

IN Boronat, Albert; Campos, Narciso; Rodriguez-Concepcion, Manuel; Rohmer, Michel; Seeman, Myriam; Valentin, Henry E.; Venkatesh, Tyamagondlu V.; Venkatramesh, Mylavarapu

PA Monsanto Technology, LLC, USA

SO PCT Int. Appl., 155 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002012478	A2	20020214	WO 2001-US24335	20010806
	WO 2002012478	C1	20020704		
	W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
	RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
	AU 2001090522	A5	20020218	AU 2001-90522	20010806
	US 2002069426	A1	20020606	US 2001-921992	20010806
PRAI	US 2000-223483P	P	20000807		
	WO 2001-US24335	W	20010806		

L7 ANSWER 2 OF 9 CAPLUS COPYRIGHT 2003 ACS

AN 2002:963266 CAPLUS

TI Stimulation of ***carotenoid*** metabolism in arbuscular mycorrhizal roots

AU Fester, Thomas; Schmidt, Diana; Lohse, Swanhild; Walter, Michael H.; Giuliano, Giovanni; Bramley, Peter M.; Fraser, Paul D.; Hause, Bettina; Strack, Dieter

CS Leibniz-Institut für Pflanzenbiochemie, Abteilung Sekundarstoffwechsel, Halle/Saale, 06120, Germany

SO Planta (2002), 216(1), 148-154

CODEN: PLANAB; ISSN: 0032-0935

PB Springer-Verlag

DT Journal

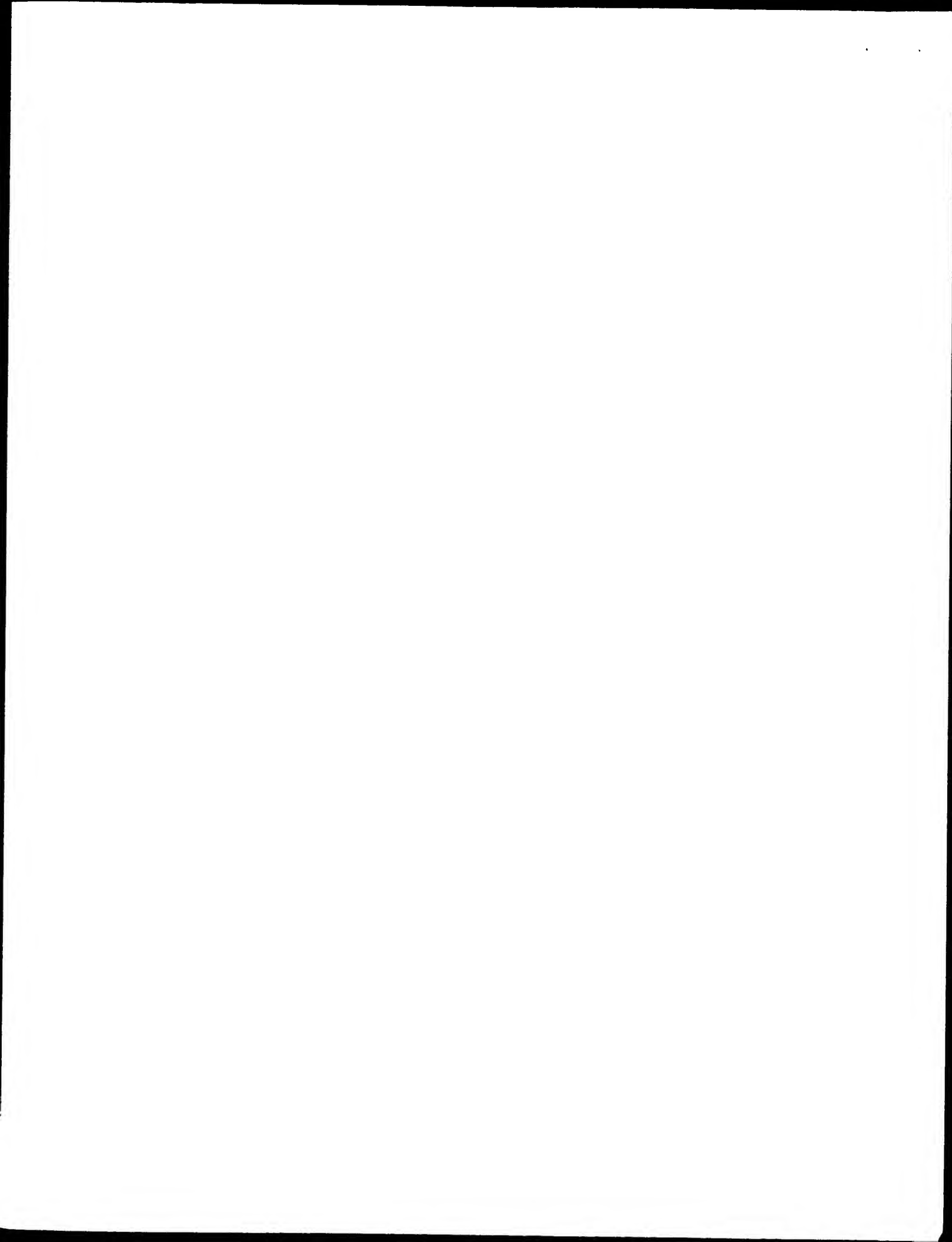
LA English

RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 3 OF 9 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 1

AN 2001:37726 BIOSIS

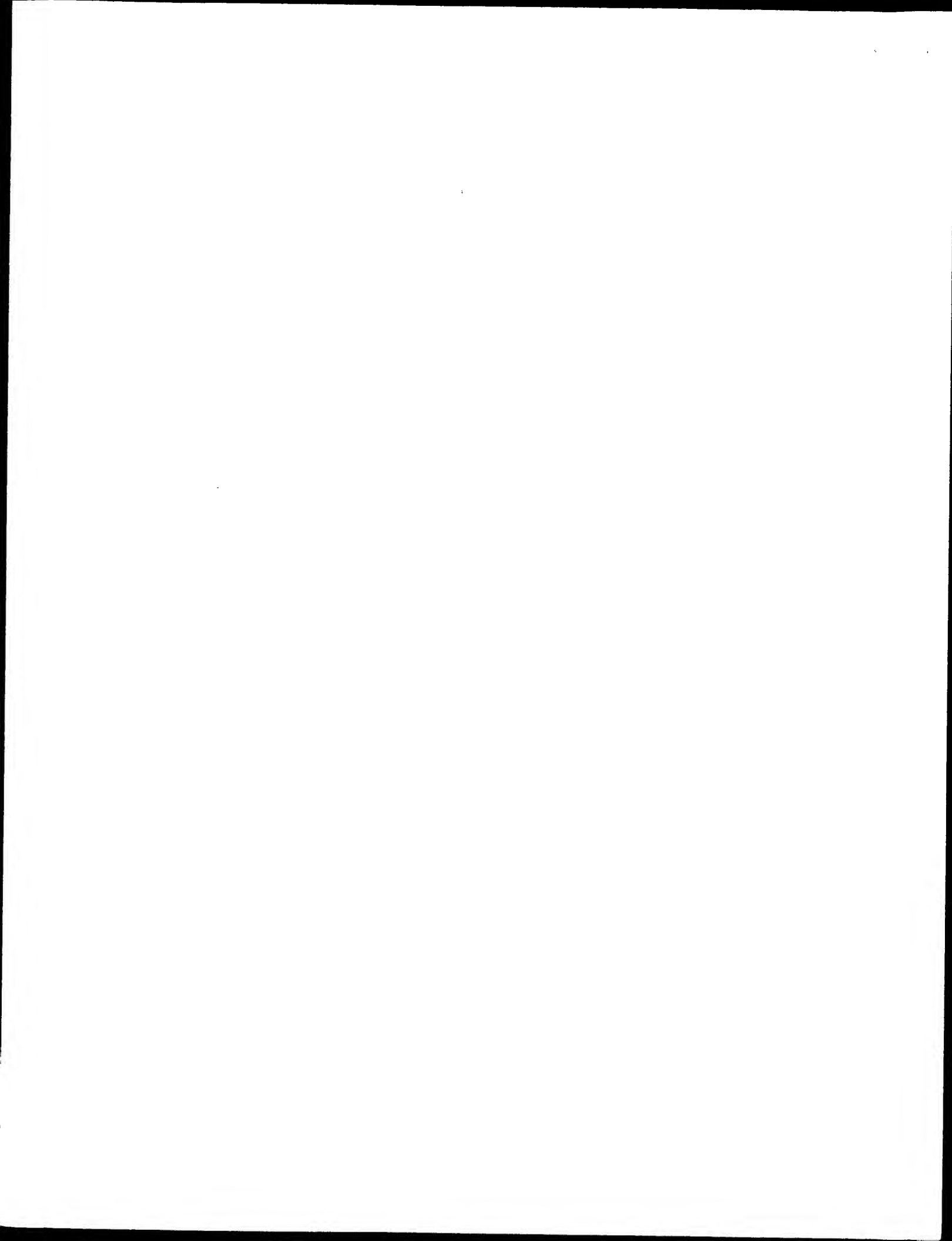


DN PREV200100037726
 TI The chloroplast and leaf developmental mutant, pale cress, exhibits light-conditional severity and symptoms characteristic of its ABA deficiency.
 AU Holding, David R. (1); Springer, Patricia S.; Coomber, Shirley A.
 CS (1) Department of Botany and Plant Sciences, University of California, Riverside, CA, 92521: dholding@ucr.edu USA
 SO Annals of Botany (London), (November, 2000) Vol. 86, No. 5, pp. 953-962. print.
 ISSN: 0305-7364.
 DT Article
 LA English
 SL English

L7 ANSWER 4 OF 9 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
 AN 2000311165 EMBASE
 TI Medicinal plant biotechnology: The Apiaceae family as the example of rapid development.
 AU Ekiert H.
 CS Dr. H. Ekiert, Dept. of Pharmaceutical Botany, Collegium Medicum, Jagiellonian University, 9 Medyczna Street, 30-688 Krakow, Poland. mfeikiert@cyf-kr.edu.pl
 SO Pharmazie, (2000) 55/8 (561-567).
 Refs: 66
 ISSN: 0031-7144 CODEN: PHARAT
 CY Germany
 DT Journal; General Review
 FS 029 Clinical Biochemistry
 LA English
 SL English

L7 ANSWER 5 OF 9 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 2
 AN 2001:49727 BIOSIS
 DN PREV200100049727
 TI Identification of a novel gene coding for neoxanthin synthase from Solanum tuberosum.
 AU Al-Babili, Salim; Hugueney, Philippe; Schledz, Michael; Welsch, Ralf; Frohnmeyer, Hanns; Laule, Oliver; Beyer, Peter (1)
 CS (1) Center for Applied Biosciences, University of Freiburg, Schaezlestr. 1, D-79104, Freiburg: beyer@uni-freiburg.de Germany
 SO FEBS Letters, (24 November, 2000) Vol. 485, No. 2-3, pp. 168-172. print.
 ISSN: 0014-5793.
 DT Article
 LA English
 SL English

L7 ANSWER 6 OF 9 CAPLUS COPYRIGHT 2003 ACS
 AN 1995:999495 CAPLUS
 DN 124:48378
 TI Studies on ***carotenoid*** biosynthesis using the methods of natural products chemistry, molecular biology, and metabolic engineering
 AU Misawa, Norihiko
 CS Cent. Lab. Key Technol., Kirin Brew. Co., Ltd., Yokohama, 236, Japan
 SO Nippon Nogei Kagaku Kaishi (1995), 69(12), 1567-72
 CODEN: NNKKA; ISSN: 0002-1407
 DT Journal; General Review
 LA Japanese



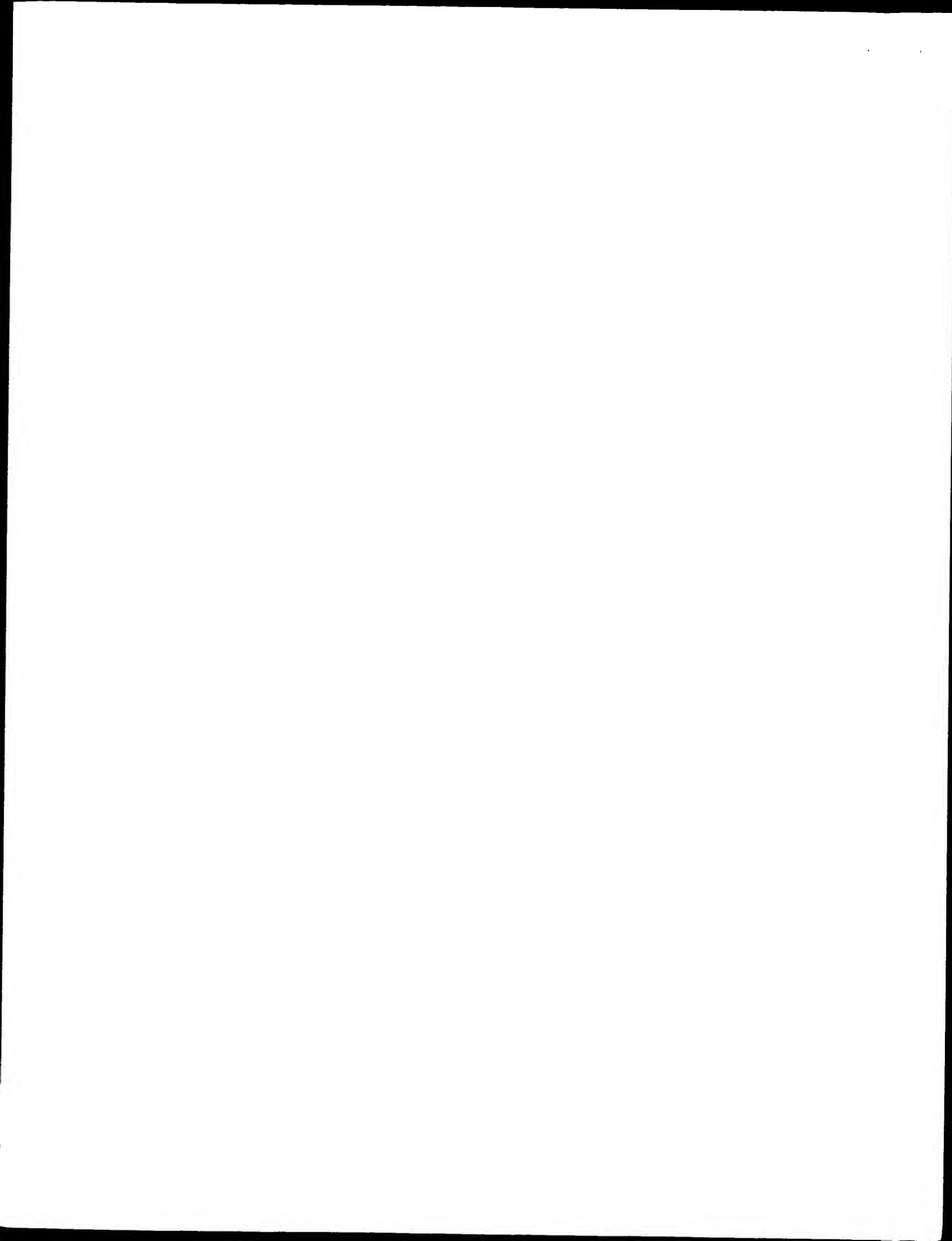
L7 ANSWER 7 OF 9 AGRICOLA DUPLICATE 3
 AN 97:60817 AGRICOLA
 DN IND20585833
 TI Constitutive expression of a fruit phytoene synthase gene in transgenic tomatoes causes dwarfism by redirecting metabolites from the gibberellin pathway.
 AU Fray, R.G.; Wallace, A.; Fraser, P.D.; Valero, D.; Hedden, P.; Bramley, P.M.; Grierson, D.
 CS Nottingham University, Loughborough, UK.
 SO The Plant journal : for cell and molecular biology, Nov 1995. Vol. 8, No. 5. p. 693-701
 Publisher: Oxford : Blackwell Scientific Publishers and BIOS Scientific Publishers in association with the Society for Experimental Biology, c1991-
 ISSN: 0960-7412
 NTE Includes references
 CY England; United Kingdom
 DT Article
 FS Non-U.S. Imprint other than FAO
 LA English

L7 ANSWER 8 OF 9 AGRICOLA DUPLICATE 4
 AN 94:73190 AGRICOLA
 DN IND20421086
 TI Engineering cyanobacterial models resistant to bleaching herbicides.
 AU Windhovel, U.; Geiges, B.; Sandmann, G.; Boger, P.
 AV DNAL (SB951.P49)
 SO Pesticide biochemistry and physiology, May 1994. Vol. 49, No. 1. p. 63-71
 Publisher: Orlando, Fla. : Academic Press.
 CODEN: PCBPBS; ISSN: 0048-3575
 NTE Includes references
 CY Florida; United States
 DT Article
 FS U.S. Imprints not USDA, Experiment or Extension
 LA English

L7 ANSWER 9 OF 9 AGRICOLA DUPLICATE 5
 AN 94:4347 AGRICOLA
 DN IND20363264
 TI Identification and genetic analysis of normal and mutant phytoene synthase genes of tomato by sequencing, complementation and co-suppression.
 AU Fray, R.G.; Grierson, D.
 AV DNAL (QK710.P62)
 SO Plant molecular biology, July 1993. Vol. 22, No. 4. p. 589-602
 Publisher: Dordrecht : Kluwer Academic Publishers.
 CODEN: PMBIDB; ISSN: 0167-4412
 NTE Includes references
 CY Netherlands
 DT Article
 FS Non-U.S. Imprint other than FAO
 LA English

=> FIL STNGUIDE
 COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION



FULL ESTIMATED COST

32.89

55.29

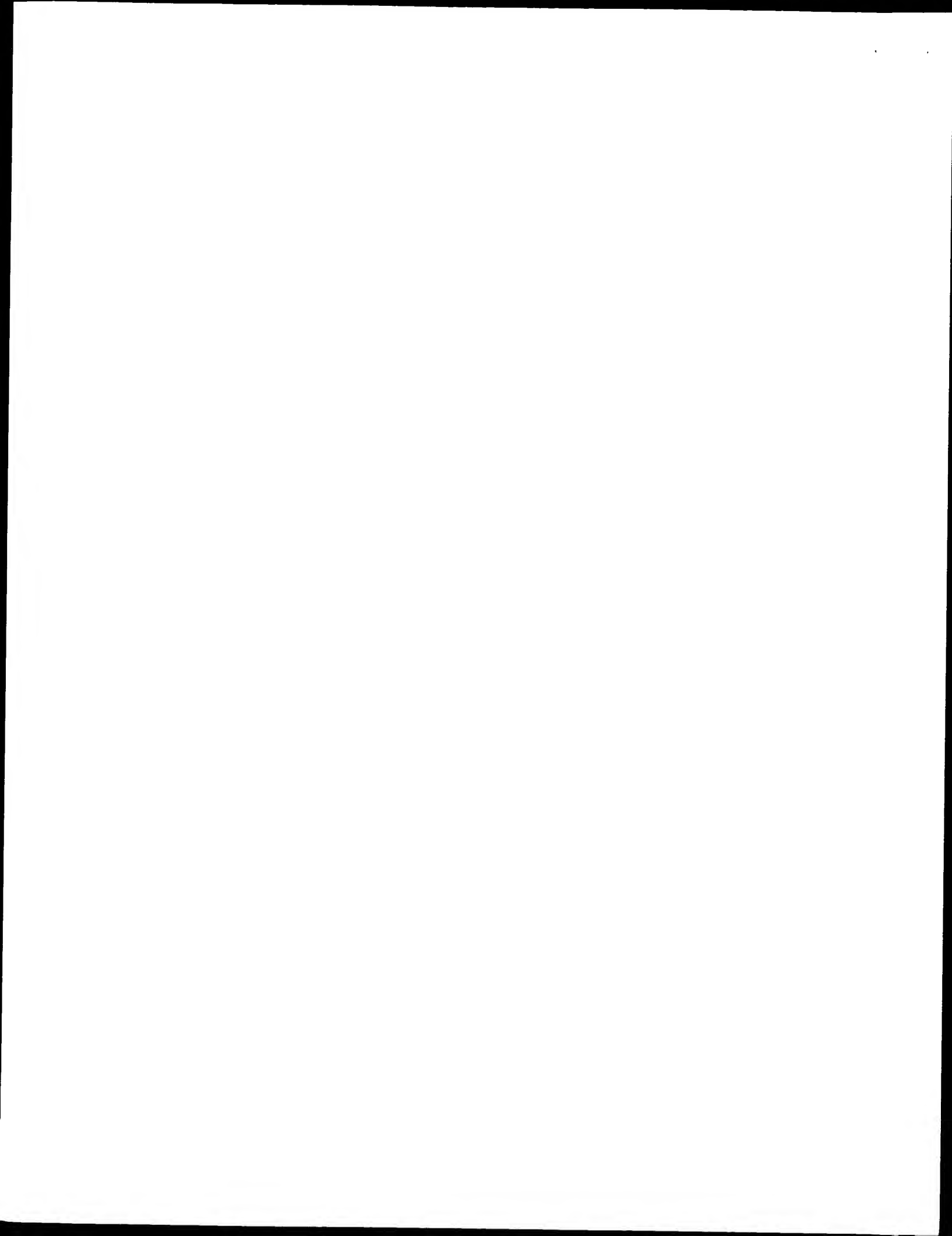
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LAST RELOADED: Feb 14, 2003 (20030214/UP).

=> d l7 7 ab ibib
YOU HAVE REQUESTED DATA FROM FILE 'AGRICOLA, BIOSIS, EMBASE, CAPLUS' - CONTINUE?
(Y)/N:y

L7 ANSWER 7 OF 9 AGRICOLA DUPLICATE 3
AB Tomato ***plants*** ***transformed*** with a copy of the
fruit-expressed phytoene synthase cDNA under control of the CaMV 355
promoter showed ectopic production of ***carotenoids***. High
expressers were reduced in stature. The dwarf character was inherited with
an inverse relationship between expression of phytoene synthase and plant
height. Severely affected plants also showed reduced chlorophyll content
in young leaves. These dwarfs showed a 30-fold reduction in levels of
gibberellin A1 (GA1) and growth was partially restored by treatment with
exogenous GA3. Qualitative and quantitative changes in ***carotenoids***
were also found. It is proposed that the dwarf phenotype results from the
over-production of phytoene synthase, which converts geranylgeranyl
diphosphate to phytoene and thereby diverts this intermediate away from
the gibberellin (GA) and phytol biosynthetic pathways.
ACCESSION NUMBER: 97:60817 AGRICOLA
DOCUMENT NUMBER: IND20585833
TITLE: Constitutive expression of a fruit phytoene synthase
gene in transgenic tomatoes causes dwarfism by
redirecting metabolites from the gibberellin pathway.
AUTHOR(S): Fray, R.G.; Wallace, A.; Fraser, P.D.; Valero, D.;
Hedden, P.; Bramley, P.M.; Grierson, D.
CORPORATE SOURCE: Nottingham University, Loughborough, UK.
SOURCE: The Plant journal : for cell and molecular biology,
Nov 1995. Vol. 8, No. 5. p. 693-701
Publisher: Oxford : Blackwell Scientific Publishers
and BIOS Scientific Publishers in association with the
Society for Experimental Biology, c1991-
ISSN: 0960-7412
NOTE: Includes references
PUB. COUNTRY: England; United Kingdom
DOCUMENT TYPE: Article
FILE SEGMENT: Non-U.S. Imprint other than FAO
LANGUAGE: English

=> s terminal(w)oxidase and carotenoid and plant
11 TERMINAL
0 OXIDASE
0 TERMINAL(W)OXIDASE
0 CAROTENOID
13 PLANT



6 PLANTS
19 PLANT
(PLANT OR PLANTS)
L8 0 TERMINAL(W)OXIDASE AND CAROTENOID AND PLANT

=> file agricola biosis embase caplus
COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
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FULL ESTIMATED COST

FILE 'AGRICOLA' ENTERED AT 18:33:18 ON 20 FEB 2003

FILE 'BIOSIS' ENTERED AT 18:33:18 ON 20 FEB 2003
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=> s terminal(w)oxidase and carotenoid and plant
L9 19 TERMINAL(W) OXIDASE AND CAROTENOID AND PLANT

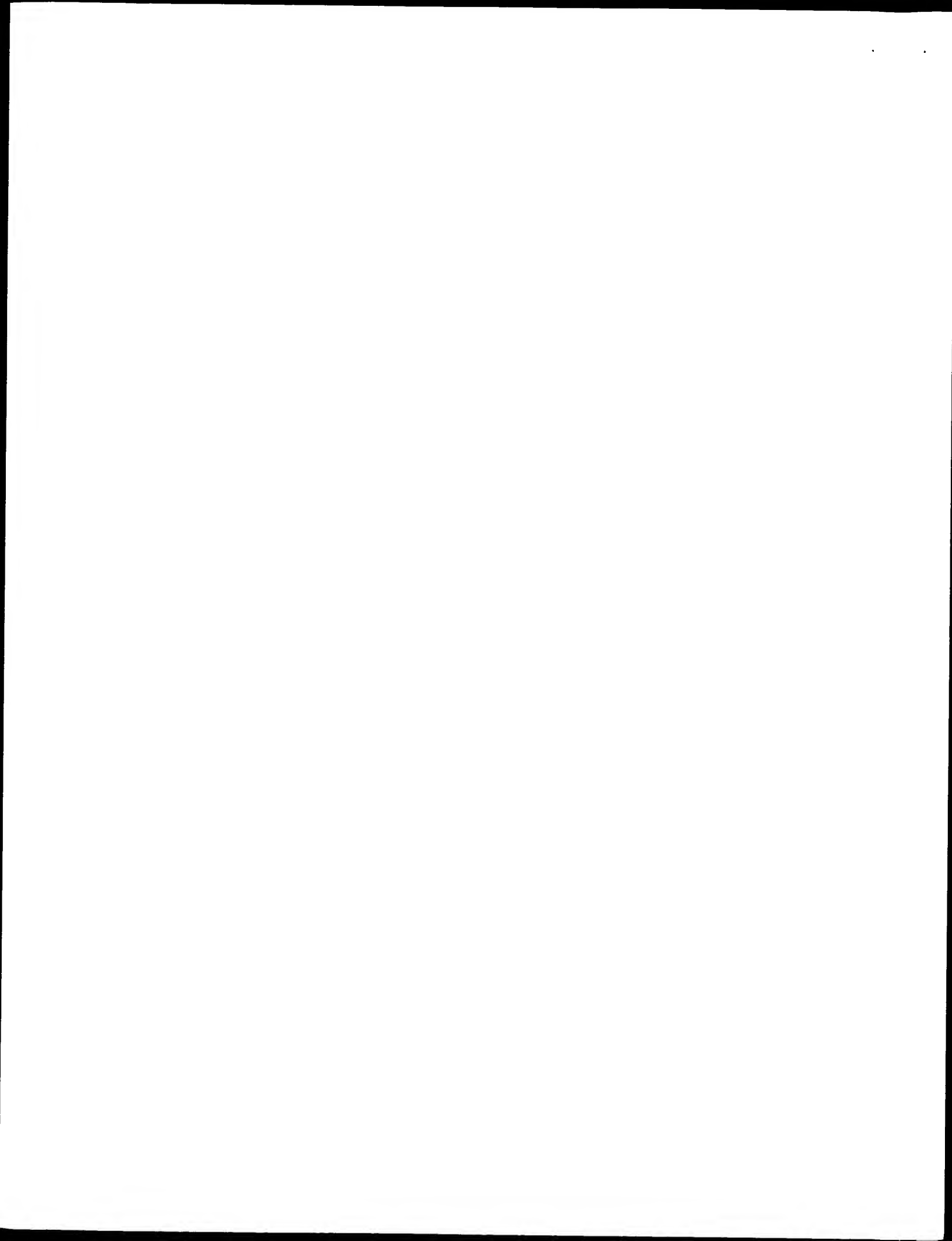
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L10 10 DUPLICATE REMOVE L9 (9 DUPLICATES REMOVED)

=> d l10 1-10

L10 ANSWER 1 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE
1
AN 2002:526871 BIOSIS
DN PREV200200526871
TI Involvement of a plastid ***terminal*** ***oxidase*** in
plastoquinone oxidation as evidenced by expression of the Arabidopsis
thaliana enzyme in tobacco.
AU Joet, Thierry; Genty, Bernard; Josse, Eve-Marie; Kuntz, Marcel; Cournac,
Laurent; Peltier, Gilles (1)
CS (1) Direction des Sciences du Vivant, Departement d'Ecophysiologie
Vegetale et de Microbiologie, Laboratoire d'Ecophysiologie de la
Photosynthese, CEA Cadarache, Unite Mixte de Recherche 163 CNRS CEA,
Univ-Mediterranee, CEA1000, 13108, Saint-Paul-lez-Durance Cedex:
gilles.peltier@cea.fr France
SO Journal of Biological Chemistry, (August 30, 2002) Vol. 277, No. 35, pp.
31623-31630. <http://www.jbc.org/>. print.
ISSN: 0021-9258.
DT Article
LA English

L10 ANSWER 2 OF 10 AGRICOLA
AN 2001:23319 AGRICOLA
DN IND22300531

DUPLICATE 2



TI A plastid ***terminal*** ***oxidase*** comes to light:
 implications for ***carotenoid*** biosynthesis and chlororespiration.
 AU Carol, P.; Kuntz, M.
 AV DNAL (QK1.T74)
 SO Trends in plant science, Jan 2001. Vol. 6, No. 1. p. 31-36
 Publisher: Kidlington, Oxford : Elsevier Science, Ltd., c1996-
 ISSN: 1360-1385
 NTE Includes references
 CY England; United Kingdom
 DT Article; Law
 FS Non-U.S. Imprint other than FAO
 LA English

L10 ANSWER 3 OF 10 CAPLUS COPYRIGHT 2003 ACS

AN 2000:278123 CAPLUS

DN 132:318612

TI Arabidopsis ***terminal*** ***oxidase*** associated with
 carotenoid biosynthesis, modification of ***plant***
 carotenoid biosynthesis, and method for herbicide screening

IN Carol, Pierre; Kuntz, Marcel; Mache, Regis

PA Universite Joseph Fourier, Fr.

SO PCT Int. Appl., 53 pp.

CODEN: PIXXD2

DT Patent

LA French

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000023605	A1	20000427	WO 1999-IB1719	19991020
	W: CA, IL, JP, US				
	RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	FR 2784688	A1	20000421	FR 1998-13283	19981020
	FR 2784688	B1	20021213		
	EP 1123406	A1	20010816	EP 1999-952734	19991020
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	JP 2002527113	T2	20020827	JP 2000-577312	19991020
PRAI	FR 1998-13283	A	19981020		
	WO 1999-IB1719	W	19991020		

RE.CNT 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 4 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.

AN 2001:56235 BIOSIS

DN PREV200100056235

TI In vitro and in situ inhibition of ***carotenoid*** biosynthesis in
 Capsicum annuum by bleaching herbicides.

AU Simkin, Andrew J.; Breitenbach, Jurgen; Kuntz, Marcel (1); Sandmann,
 Gerhard

CS (1) Genetique Moleculaire des Plantes, CNRS (UMR5575), Universite J.
 Fourier, F-38041, Grenoble Cedex, 9: marcel.kuntz@ujf-grenoble.fr France

SO Journal of Agricultural and Food Chemistry, (October, 2000) Vol. 48, No.
 10, pp. 4676-4680. print.

ISSN: 0021-8561.

DT Article

LA English

SL English

L10 ANSWER 5 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE
3

AN 2000:452024 BIOSIS

DN PREV200000452024

TI A plastid ***terminal*** ***oxidase*** associated with
carotenoid desaturation during chromoplast differentiation.

AU Josse, Eve-Marie; Simkin, Andrew J.; Gaffe, Joel; Laboure, Anne-Marie;
Kuntz, Marcel (1); Carol, Pierre

CS (1) Laboratoire de Genetique Moleculaire des Plantes, Unite Mixte de
Recherche 5575, Universite Joseph Fourier, Centre National de la Recherche
Scientifique, 38041, Grenoble Cedex 9 France

SO Plant Physiology (Rockville), (August, 2000) Vol. 123, No. 4, pp.
1427-1436. print.

ISSN: 0032-0889.

DT Article

LA English

SL English

L10 ANSWER 6 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.

AN 2000:533098 BIOSIS

DN PREV200000533098

TI A plastid ***terminal*** ***oxidase*** associated with
carotenoid desaturation during chromoplast differentiation.

AU Josse, E.-M. (1); Simkin, A. J. (1); Gaffe, J. (1); Laboure, A.-M. (1);
Kuntz, M. (1); Carol, P. (1)

CS (1) Laboratoire de Genetique Moleculaire des Plantes, Universite Joseph
Fourier and CNRS (UMR 5575), 38041, Grenoble Cedex 9 France

SO Plant Physiology and Biochemistry (Paris), (August, 2000) Vol. 38, No.
Supplement, pp. s265. print.

Meeting Info.: 12th Congress of the Federation of European Societies of
Plant Physiology Budapest, Hungary August 21-25, 2000

ISSN: 0981-9428.

DT Conference

LA English

SL English

L10 ANSWER 7 OF 10 AGRICOLA

DUPLICATE 4

AN 1999:59000 AGRICOLA

DN IND21996880

TI Mutations in the Arabidopsis gene IMMUTANS cause a variegated phenotype by
inactivating a chloroplast ***terminal*** ***oxidase*** associated
with phytoene desaturation.

AU Carol, P.; Stevenson, D.; Bisanz, C.; Breitenbach, J.; Sandmann, G.;
Mache, R.; Coupland, G.; Kuntz, M.

CS Universite Joseph Fourier, Grenoble, France.

AV DNAL (QK725.P532)

SO The Plant cell, Jan 1999. Vol. 11, No. 1. p. 57-68

Publisher: [Rockville, MD : American Society of Plant Physiologists,
c1989-

CODEN: PLCEEW; ISSN: 1040-4651

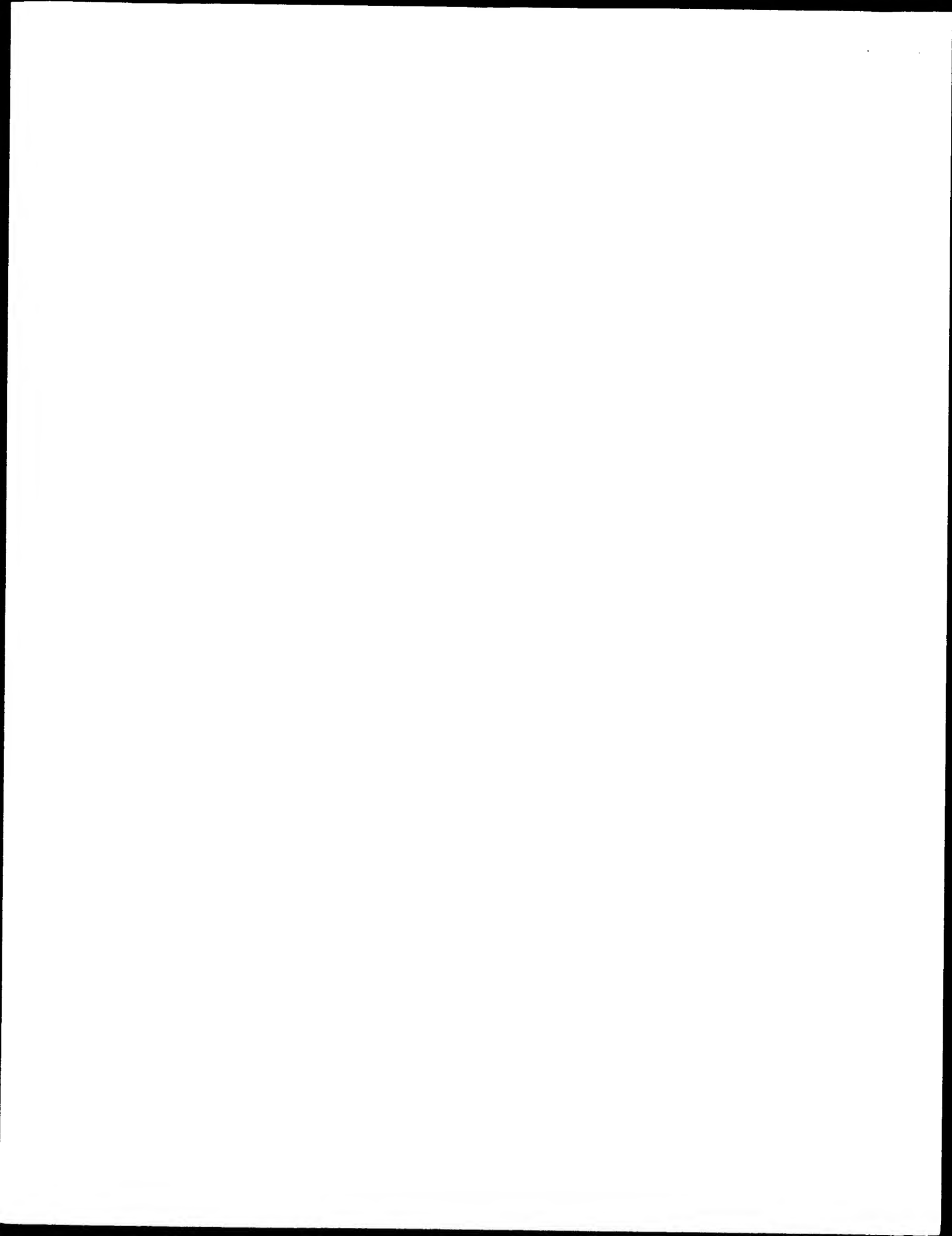
NTE Includes references

CY Maryland; United States

DT Article

FS U.S. Imprints not USDA, Experiment or Extension

LA English



L10 ANSWER 8 OF 10 AGRICOLA DUPLICATE 5
 AN 1999:58999 AGRICOLA
 DN IND21996873
 TI The IMMUTANS variegation locus of Arabidopsis defines a mitochondrial alternative oxidase homology that functions during early chloroplast biogenesis.
 AU Wu, D.; Wright, D.A.; Wetzel, C.; Voytas, D.F.; Rodermel, D.
 CS Iowa State University, Ames, IA.
 AV DNAL (QK725.P532)
 SO The Plant cell, Jan 1999. Vol. 11, No. 1. p. 43-55
 Publisher: [Rockville, MD : American Society of Plant Physiologists, c1989-
 CODEN: PLCEEW; ISSN: 1040-4651
 NTE Includes references
 CY Maryland; United States
 DT Article
 FS U.S. Imprints not USDA, Experiment or Extension
 LA English

L10 ANSWER 9 OF 10 CAPLUS COPYRIGHT 2003 ACS
 AN 1963:476714 CAPLUS
 DN 59:76714
 OREF 59:14302a-d
 TI Dependence of oxygen absorption by green and nongreen leaves on the intensity and spectral composition of light
 AU Voskresenskaya, N. P.
 SO Fiziol. Drevesn. Rastanii (or:Moscow: Akad. Nauk SSSR (1962) 150-9
 From: Ref. Zh., Biol. Khim. 1963, Abstr. No. 11F704.
 DT Journal
 LA Unavailable

L10 ANSWER 10 OF 10 CAPLUS COPYRIGHT 2003 ACS
 AN 1961:138228 CAPLUS
 DN 55:138228
 OREF 55:26143h-i,26144a
 TI Effect of shortwave radiation on absorption of oxygen by ***plant*** leaves
 AU Voskresenskaya, N. P.
 CS K. A. Timiryazev Inst. Plant Physiol., Moscow
 SO Problemy Fotosinteza, Doklady 2-oi [Vtoroi] Konf., Moscow (1959), Volume Date 1957 335-45
 DT Journal
 LA Unavailable

=> FIL STNGUIDE

COST IN U.S. DOLLARS

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FULL ESTIMATED COST

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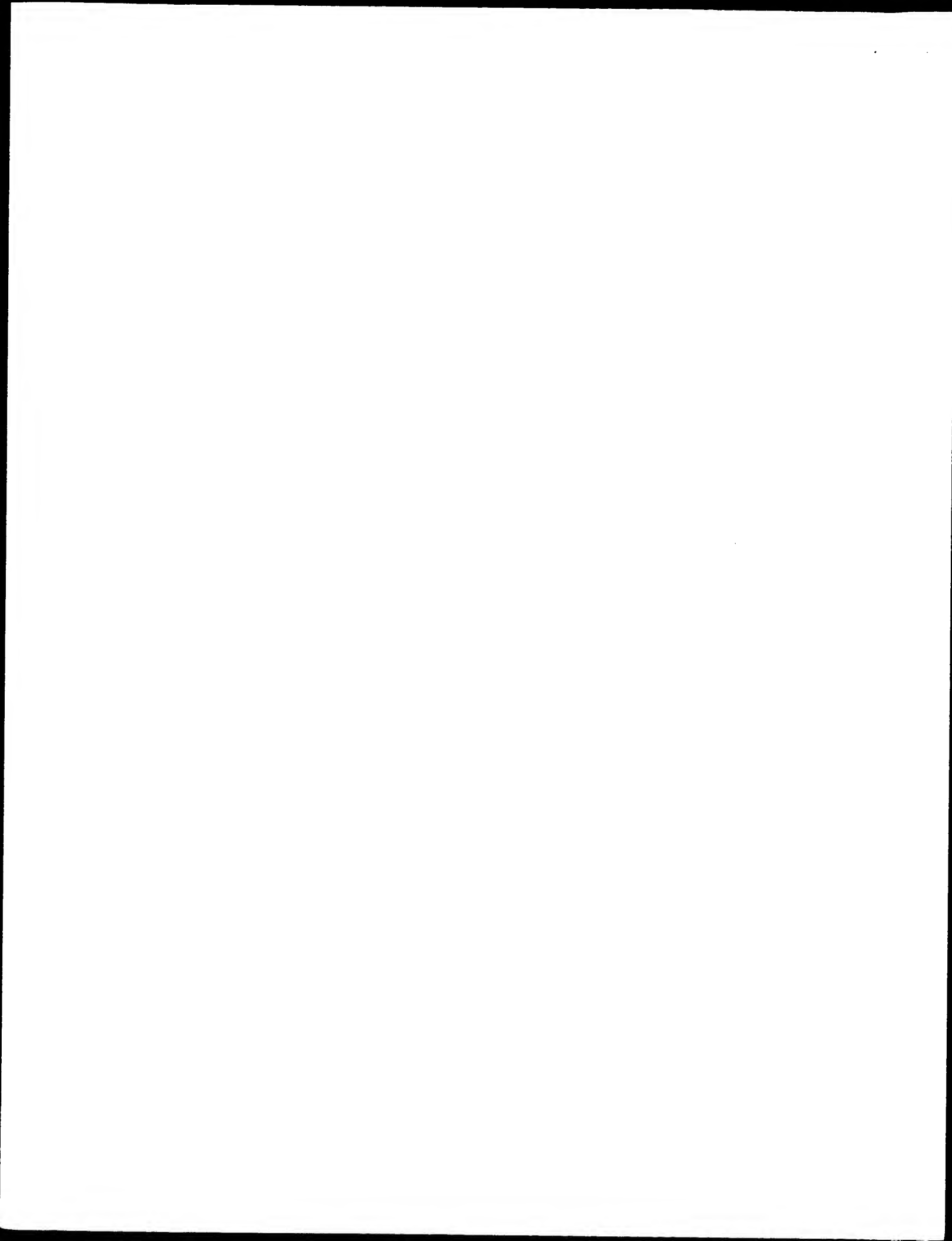
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AND TECHNOLOGY CORPORATION, AND FACHINFORMATIONSZENTRUM KARLSRUHE

FILE CONTAINS CURRENT INFORMATION.



LAST RELOADED: Feb 14, 2003 (20030214/UP).

=> s carotenoid and transform?

0 CAROTENOID

0 TRANSFORM?

L11 0 CAROTENOID AND TRANSFORM?

=> file agricola biosis embase caplus

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

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=> s carotenoid and transform?

L12 1307 CAROTENOID AND TRANSFORM?

=> s l12 and plant

L13 370 L12 AND PLANT

=> duplicate remove l13

DUPLICATE PREFERENCE IS 'AGRICOLA, BIOSIS, EMBASE, CAPLUS'

KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n

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L14 287 DUPLICATE REMOVE L13 (83 DUPLICATES REMOVED)

=> s l14 and transgenic

L15 61 L14 AND TRANSGENIC

=> d l15 51-61

L15 ANSWER 51 OF 61 CAPLUS COPYRIGHT 2003 ACS

AN 1996:637967 CAPLUS

DN 125:294058

TI Use of gene silencing to probe ***carotenoid*** gene expression in
tomato

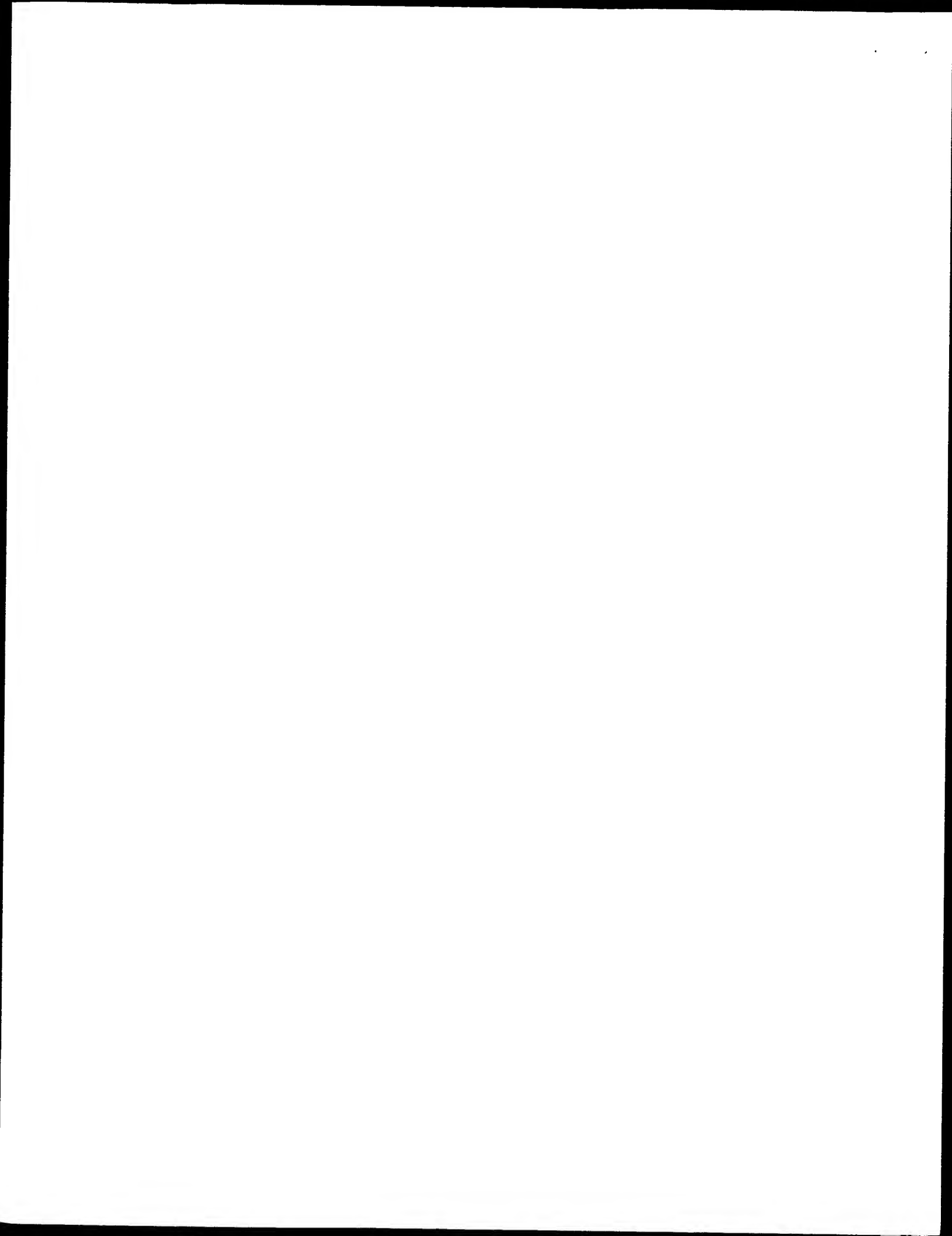
AU Fray, R. G.; Hamilton, A. J.; Grierson, D.; Davey, M. R.; Blackhall, N. W.

CS Dep. of Physiology and Environmental Science, Univ. of Nottingham, Leics,
UK

SO Mechanisms and Applications of Gene Silencing, [Easter School in
Agricultural Science], 57th, Sutton Bonington, UK, Mar., 1995 (1996),
Meeting Date 1995, 49-55, 8 plates. Editor(s): Grierson, Donald; Lycett,
Grantley W.; Tucker, Gregory A. Publisher: Nottingham University Press,
Nottingham, UK.

CODEN: 63NBAT

DT Conference; General Review



LA English

L15 ANSWER 52 OF 61 CAPLUS COPYRIGHT 2003 ACS

AN 1996:481698 CAPLUS

DN 125:137740

TI Manipulating ***carotenoids*** in ***transgenic*** ***plants***

AU Schuch, Wolfgang; Drake, Rachel; Romer, Susanne; Bramley, Peter M.

CS Zeneca Plant Science, Jealott's Hill Research Station,
Bracknell/Berkshire, RG42 6EY, UK

SO Annals of the New York Academy of Sciences (1996), 792 (Engineering Plants
for Commercial Products and Applications), 13-19

CODEN: ANYAA9; ISSN: 0077-8923

PB New York Academy of Sciences

DT Journal; General Review

LA English

L15 ANSWER 53 OF 61 CAPLUS COPYRIGHT 2003 ACS

AN 1996:410595 CAPLUS

DN 125:82197

TI Increasing yields of ***carotenoids*** in ***plants*** by
expression of genes for microbial phytoene synthases in storage organs

IN Hauptmann, Randal; Eschenfeldt, William H.; English, Jami; Brinkhaus,
Friedhelm L.

PA Amoco Corporation, USA

SO PCT Int. Appl., 105 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9613149	A1	19960509	WO 1995-US13937	19951027
	W: AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, JP, KE, KG,				
	KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MN, MW, MX, NO, NZ, PL,				
	RO, RU, SD, SI, SK, TJ, TT, UA, UZ, VN				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	CA 2203815	AA	19960509	CA 1995-2203815	19951027
	AU 9539701	A1	19960523	AU 1995-39701	19951027
	AU 697358	B2	19981001		
	EP 792352	A1	19970903	EP 1995-937660	19951027
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
	CN 1172416	A	19980204	CN 1995-197153	19951027
	PL 182161	B1	20011130	PL 1995-319788	19951027
PRAI	US 1994-331004	A	19941028		
	WO 1995-US13937	W	19951027		

L15 ANSWER 54 OF 61 CAPLUS COPYRIGHT 2003 ACS

AN 1995:1004323 CAPLUS

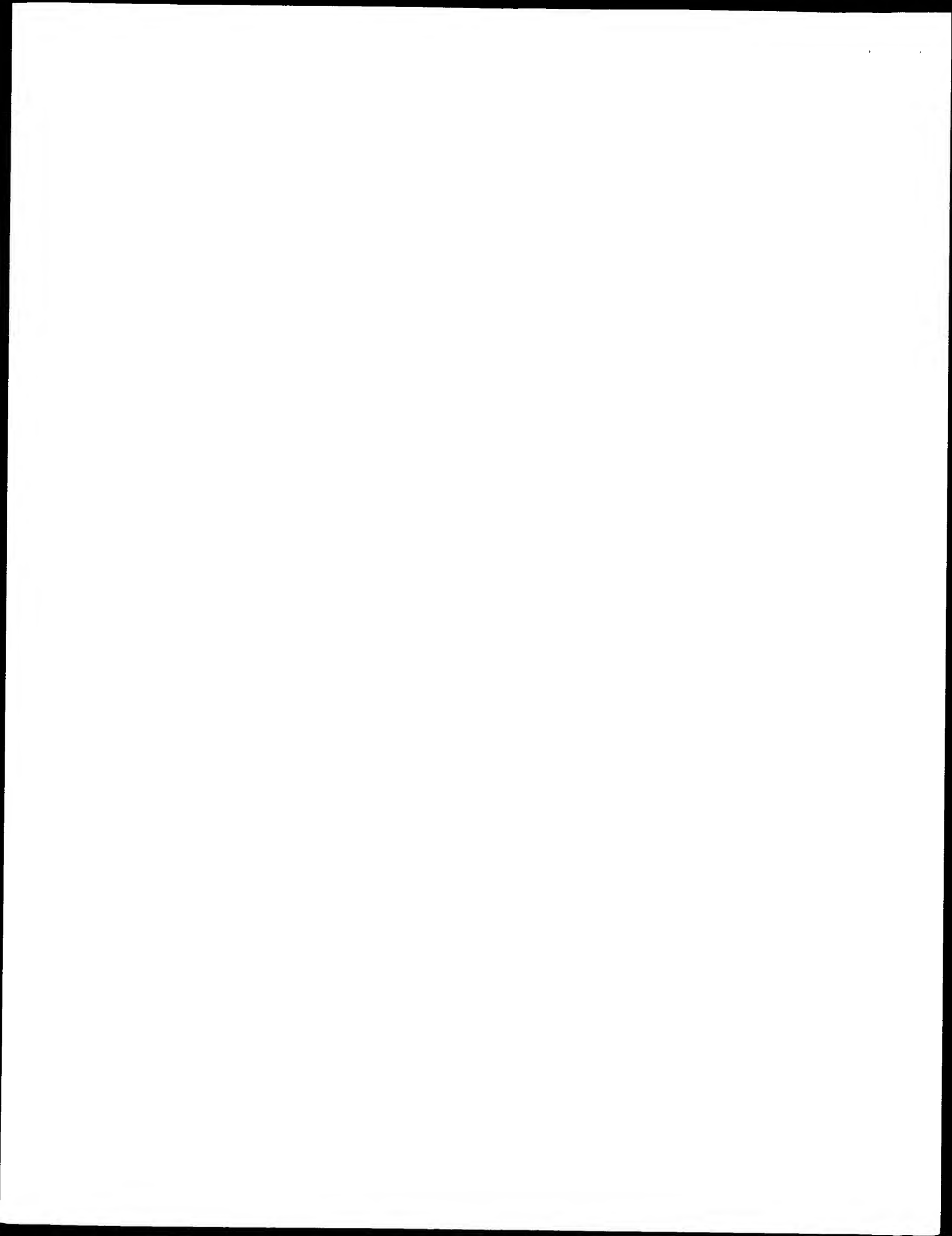
DN 124:50735

TI Is the reaction catalyzed by 3-hydroxy-3-methylglutaryl coenzyme A
reductase a rate-limiting step for isoprenoid biosynthesis in
plants ?

AU Chappell, Joseph; Wolf, Fred; Proulx, Jeanne; Cuellar, Rick; Saunders,
Court

CS Plant Physiology/Biochemistry/Molecular Biology Program, University of
Kentucky, Lexington, KY, 40546-0091, USA

SO Plant Physiology (1995), 109(4), 1337-43



CODEN: PLPHAY; ISSN: 0032-0889

PB American Society of Plant Physiologists
DT Journal
LA English

L15 ANSWER 55 OF 61 CAPLUS COPYRIGHT 2003 ACS

AN 1995:742328 CAPLUS

DN 123:139151

TI Violaxanthin cycle pigment contents in potato and tobacco ***plants***
with genetically reduced photosynthetic capacity

AU Bilger, Wolfgang; Fisahn, Joachim; Brummet, Wolfgang; Kossmann, Jens;
Willmitzer, Lothar

CS Julius-von-Sachs-Inst. Biowissenschaften, Lehrstuhl Botanik II, Wuerzburg,
97082, Germany

SO Plant Physiology (1995), 108(4), 1479-86

CODEN: PLPHAY; ISSN: 0032-0889

PB Dekker

DT Journal

LA English

L15 ANSWER 56 OF 61 CAPLUS COPYRIGHT 2003 ACS

AN 1994:428078 CAPLUS

DN 121:28078

TI Functional expression of the Erwinia uredovora ***carotenoid***
biosynthesis gene crtI in ***transgenic*** ***plants*** showing an
increase of .beta.-carotene biosynthesis activity and resistance to the
bleaching herbicide norflurazon. [Erratum to document cited in
CA120(17):209642b]

AU Misawa, Norihiko; Yamano, Shigeyuki; Linden, Hartmut; de Felipe, Maria R.;
Lucas, Mercedes; Ikenaga, Hiroshi; Sandmann, Gerhard

CS Cent. Lab. Key Technol., Kirin Brew. Co., Ltd., Yokohma, 236, Japan

SO Plant Journal (1994), 5(2), 309

CODEN: PLJUED; ISSN: 0960-7412

DT Journal

LA English

L15 ANSWER 57 OF 61 CAPLUS COPYRIGHT 2003 ACS

AN 1994:209642 CAPLUS

DN 120:209642

TI Functional expression of the Erwinia uredovora ***carotenoid***
biosynthesis gene crtI in ***transgenic*** ***plants*** showing an
increase of .beta.-carotene biosynthesis activity and resistance to the
bleaching herbicide norflurazon

AU Misawa, Norihiko; Yamano, Shigeyuki; Linden, Hartmut; de Felipe, Maria R.;
Lucas, Mercedes; Ikenaga, Hiroshi; Sandmann, Gerhard

CS Cent. Lab. Key Technol., Kirin Brew. Co., Ltd, Yokohama, 236, Japan

SO Plant Journal (1993), 4(5), 833-40

CODEN: PLJUED; ISSN: 0960-7412

DT Journal

LA English

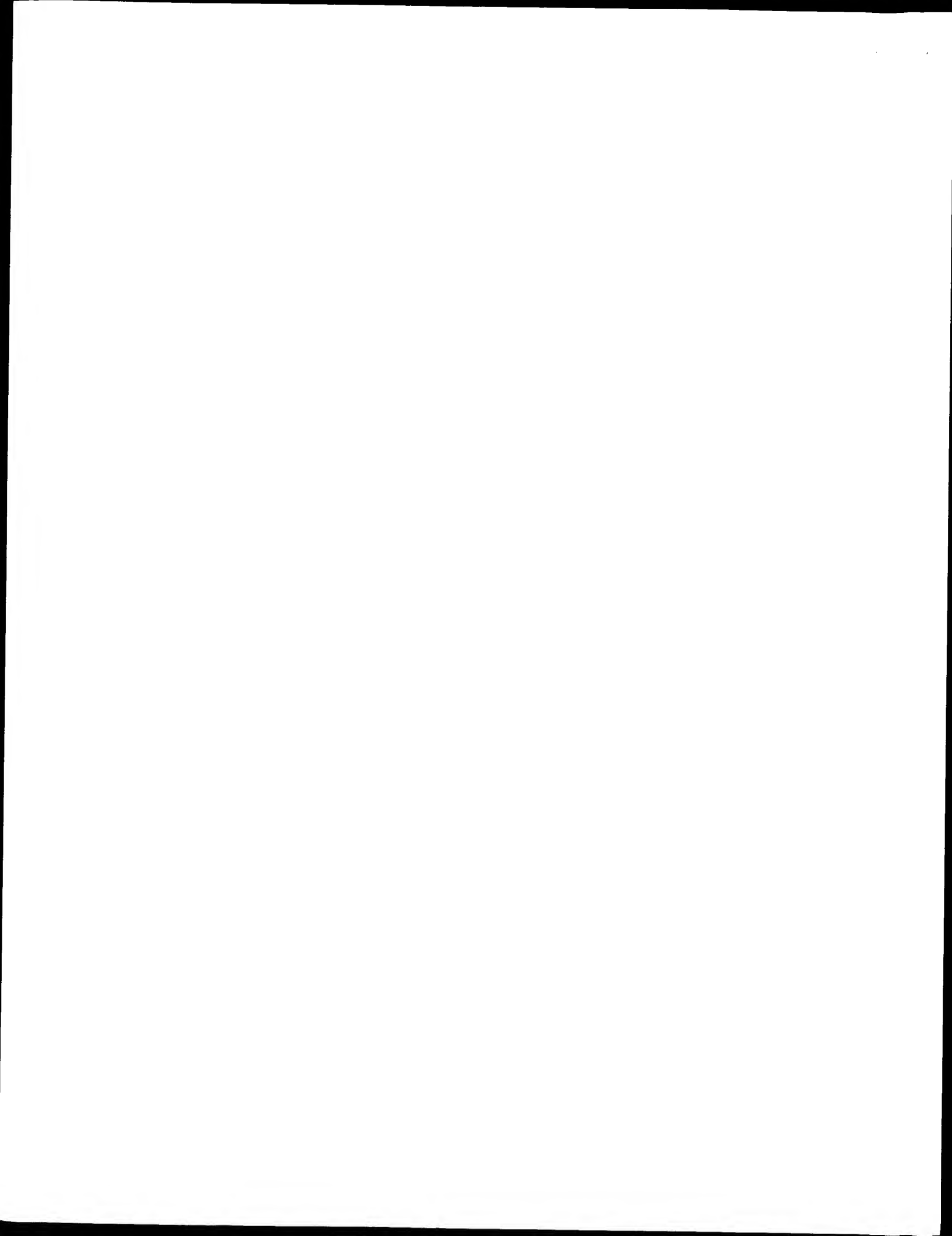
L15 ANSWER 58 OF 61 CAPLUS COPYRIGHT 2003 ACS

AN 1994:158389 CAPLUS

DN 120:158389

TI Study on the ***carotenoid*** biosynthetic pathway at the level of the
genes and enzymes

AU Misawa, N.; Yamano, S.; Kobayashi, K.; Ikenaga, H.; Nakagawa, M.;



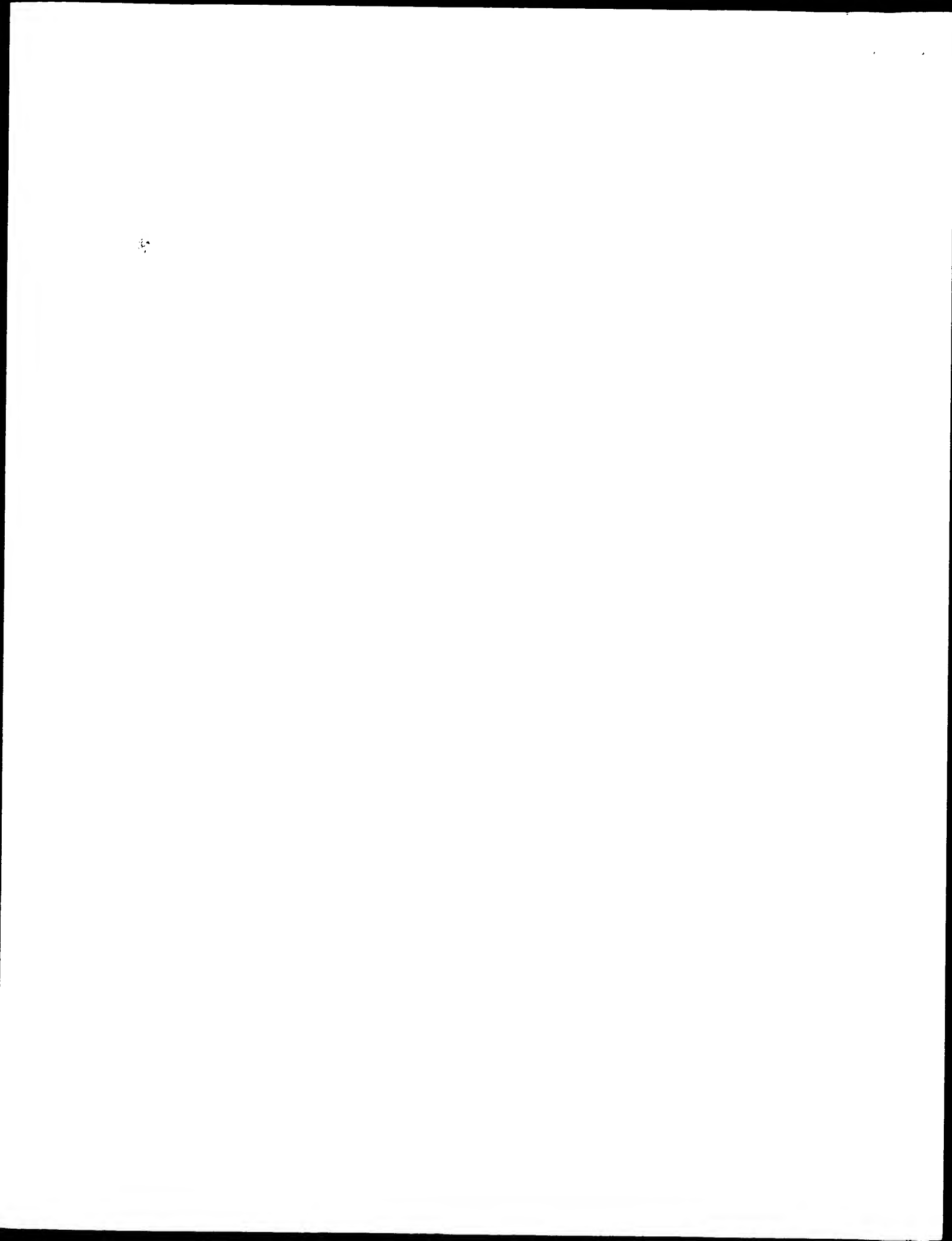
Harashima, K.; Sandmann, G.; Linden, H.
 CS Cent. Lab., Key Tech. Kirin Brewery Co., Ltd., Japan
 SO Tennen Yuki Kagobutsu Toronkai Koen Yoshishu (1992), 34th, 212-219
 CODEN: TYKYDS
 DT Journal
 LA Japanese

L15 ANSWER 59 OF 61 CAPLUS COPYRIGHT 2003 ACS
 AN 1992:35644 CAPLUS
 DN 116:35644
 TI Biosynthesis of ***carotenoids*** in genetically engineered hosts
 IN Ausich, Rodney Lee; Brinkhaus, Friedhelm Luetke; Mukharji, Indrani;
 Proffitt, John Houston; Yarger, James Gregory; Yen, Huei Che Bill
 PA Amoco Corp., USA
 SO PCT Int. Appl., 311 pp.
 CODEN: PIXXD2
 DT Patent
 LA English
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9113078	A1	19910905	WO 1991-US1458	19910304
	W: CA, JP				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LU, NL, SE				
	EP 471056	A1	19920219	EP 1991-905713	19910304
	EP 471056	B1	20011017		
	R: BE, CH, DE, DK, FR, GB, IT, LI, NL				
	JP 05504686	T2	19930722	JP 1991-506139	19910304
	US 5545816	A	19960813	US 1993-93577	19930719
	US 5530188	A	19960625	US 1993-95726	19930721
	US 5530189	A	19960625	US 1993-96043	19930722
	US 5684238	A	19971104	US 1993-96623	19930722
	US 5656472	A	19970812	US 1995-473512	19950607
PRAI	US 1990-487613	A	19900302		
	US 1990-525551	A	19900518		
	US 1990-562674	A	19900803		
	US 1991-662921	A	19910228		
	WO 1991-US1458	U	19910304		
	US 1991-785566	B1	19911030		
	US 1991-785568	B1	19911030		
	US 1991-785569	B1	19911030		
	US 1991-805061	B1	19911209		
	US 1993-95726	A3	19930721		

L15 ANSWER 60 OF 61 CAPLUS COPYRIGHT 2003 ACS
 AN 1991:649578 CAPLUS
 DN 115:249578
 TI Effects of sense and antisense transcripts of lycopene biosynthesis gene
 on fruit and flower color
 IN Bird, Colin Roger; Grierson, Donald; Schuch, Wolfgang Walter
 PA Imperial Chemical Industries PLC, UK
 SO PCT Int. Appl., 31 pp.
 CODEN: PIXXD2
 DT Patent
 LA English
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI  WO 9109128      A1  19910627      WO 1990-GB1924      19901210
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      LU, ML, MR, NL, SE, SN, TD, TG
    CA 2070831      AA  19910614      CA 1990-2070831      19901210
    AU 9168938      A1  19910718      AU 1991-68938        19901210
    AU 645534       B2  19940120
    EP 505405       A1  19920930      EP 1991-900277      19901210
    R:  AT, BE, CH, DE, DK, ES, FR, GB, IT, LI, LU, NL, SE
    JP 05502160     T2  19930422      JP 1991-500993      19901210
    EP 699765       A1  19960306      EP 1995-111177      19901210
    R:  AT, BE, CH, DE, DK, ES, FR, GB, IT, LI, LU, NL, SE
    US 5304478      A   19940419      US 1992-995950      19921228
    US 5750865      A   19980512      US 1994-300582      19940902
PRAI GB 1989-28179      19891213
    EP 1991-900277      19901210
    WO 1990-GB1924      19901210
    US 1990-625664      19901213
    US 1992-859523      19920812

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L15  ANSWER 61 OF 61  CAPLUS  COPYRIGHT 2003 ACS
AN   1988:164906  CAPLUS
DN   108:164906
TI   A DNA-liposome transfection product in pea with pigment changes
AU   Ahokas, Hannu
CS   Dep. Genet., Univ. Helsinki, Helsinki, SF-00100, Finland
SO   Annales Botanici Fennici (1987), 24(3), 245-50
      CODEN: ABOFAQ; ISSN: 0003-3847
DT   Journal
LA   English

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FULL ESTIMATED COST                21.10      103.65

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LAST RELOADED: Feb 14, 2003 (20030214/UP).

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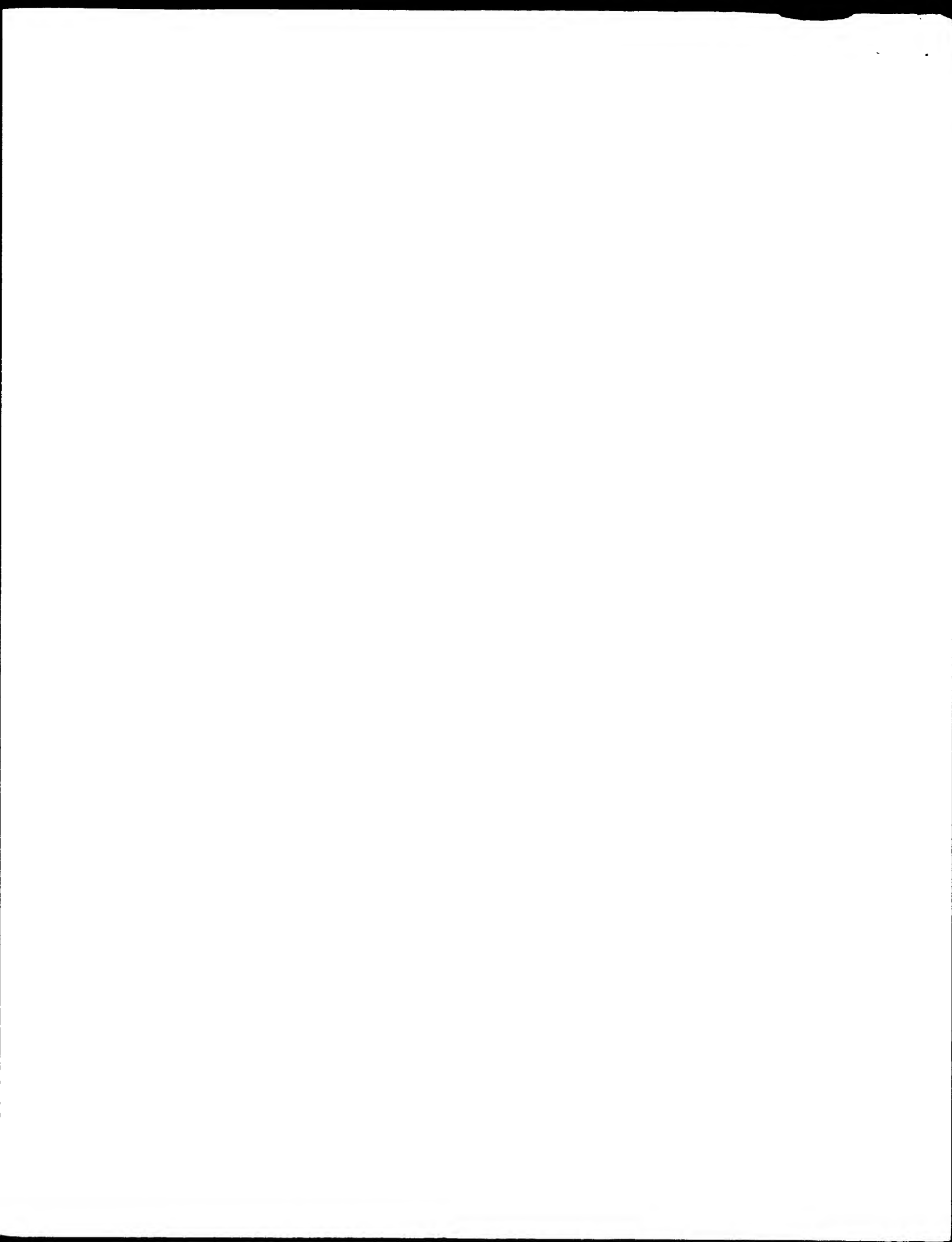
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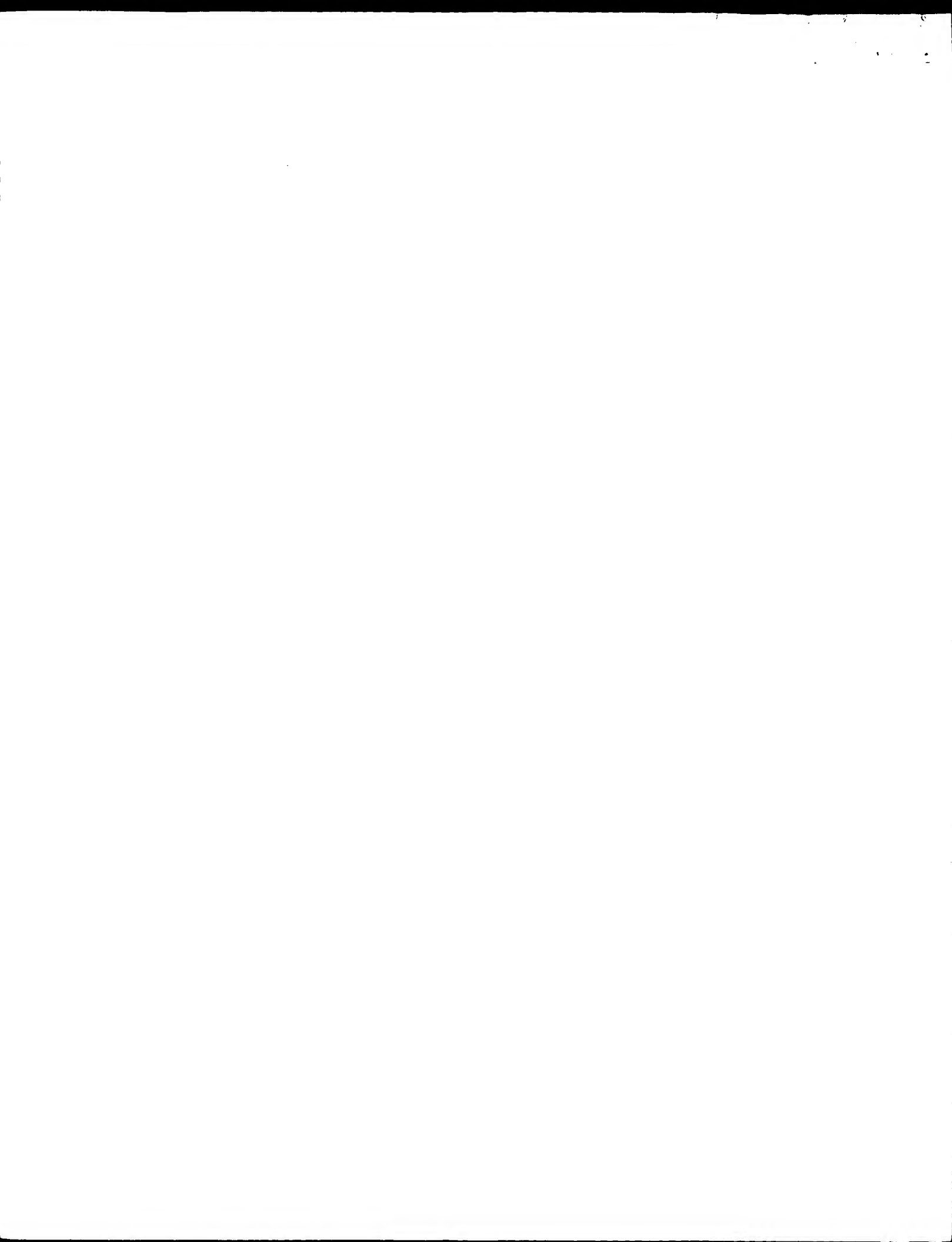
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FULL ESTIMATED COST

0.18

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JOURNAL Submitted (18-WAR-1998) Carol P., Genetique Moleculaire des
Plantes, Universite Joseph Fourier, Cermo, 460 rue de la Piscine,
Saint Martin d'heres, 38053, FRANCE

REFERENCE 2 (bases 1 to 1396)

AUTHORS Carol.P., Stevenson,D., Kuntz,M., Coupland,G. and Maché,R.

TITLE The immutans locus of arabidopsis encodes a chloroplast alternative
oxidase-like protein involved in phytoene desaturation

JOURNAL Plant Cell

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RADYLKVHPAESNMHHULLIMELGGSWMFDRFLAQHIATFYFTMTVFLYLISPRM
AYHFSECVSHAVETYVDKFELKASGEELKNMPADIAVKYTGDLXLFDEFQTSRTEN
TRRPVENLZYDVNRIDDEAEHCKTMACQTLSLSPHSFILDDDDTEESGCVCVPE
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BASE COUNT 417 a 261 c 294 g 424 t

ORIGIN

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Best Local Similarity 100.0%; Pred No. 0;
Matches 1396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGTCACATTGGGATTCGTCTTTCTTCTAAAACCCGCAAAATTTCTCCATTCTTAC 60
Db 1 CGCGTCACATTGGGATTCGTCTTTCTTCTAAAACCCGCAAAATTTCTCCATTCTTAC 60

QY 61 CAAAAATATCCAACPTTTACTTTTTCTTCTGTGAATATTCGTCAATCTTTGGTTC 120
Db 61 CAAAAATATCCAACPTTTACTTTTTCTTCTGTGAATATTCGTCAATCTTTGGTTC 120

QY 121 CTGACGGAGATGGCGCGGATTCAGGCATCTCCTGTGTGACGATTCACGGCT 180
Db 121 CTGACGGAGATGGCGCGGATTCAGGCATCTCCTGTGTGACGATTCACGGCT 180

QY 181 TTGGTTACTCTTCGAGCTCTAGAGCCGCGTTTCGTACAGCTCCTCTCACGATTCGTT 240
Db 181 TTGGTTACTCTTCGAGCTCTAGAGCCGCGTTTCGTACAGCTCCTCTCACGATTCGTT 240

QY 241 CATCATCTTCCCCTCTCTCTTCGTCGTCTGCTATTAAAGAACAAATCATCGAGTCCAAGCA 300
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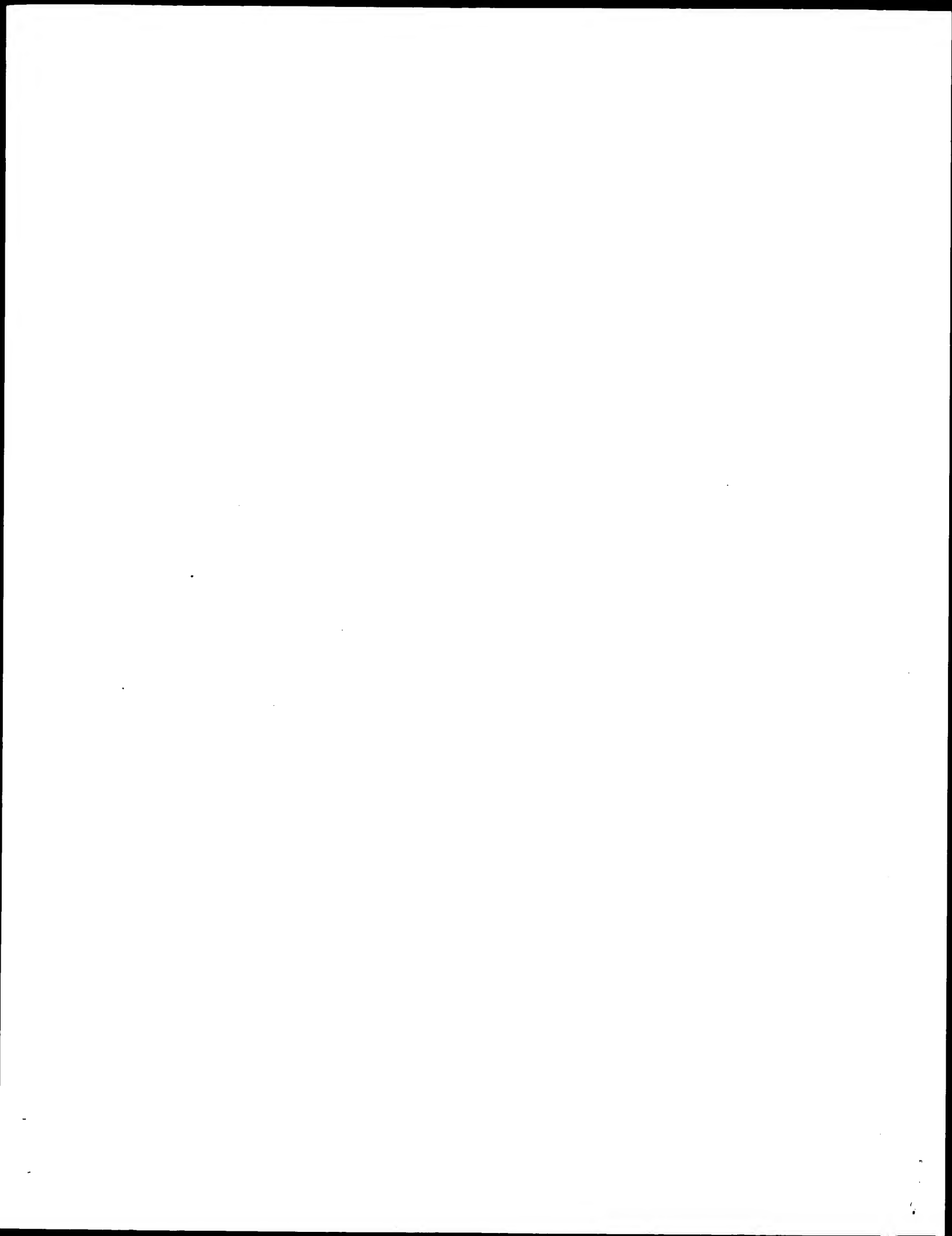
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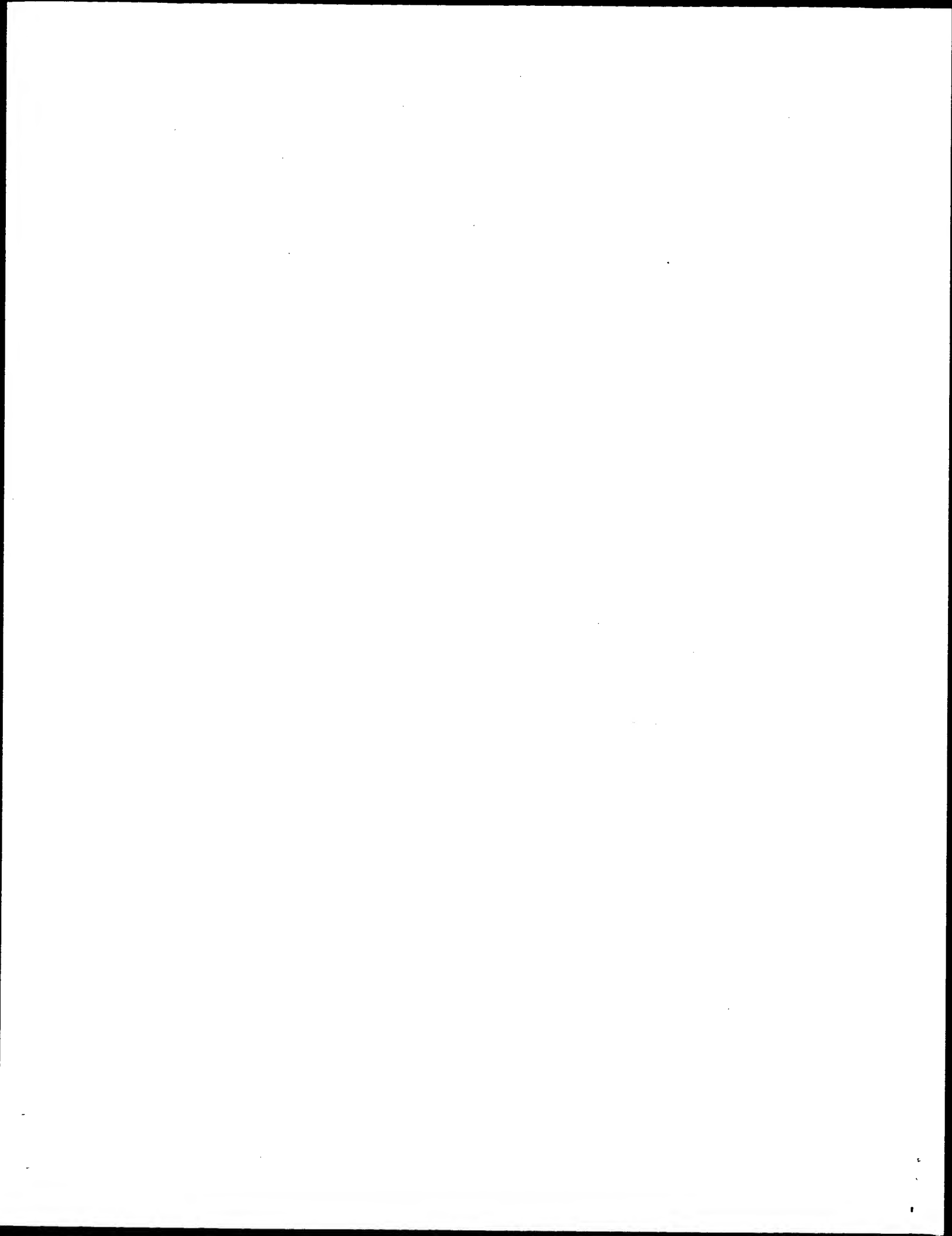
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QY 481 AAGATACTTGACACTTTGTATCGTGACCGACACATATCGAAGTTCTTTGTCTTGAGACA 540
Db 481 AAGATACTTGACACTTTGTATCGTGACCGACACATATCGAAGTTCTTTGTCTTGAGACA 540

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Best Local Similarity	99.9%;	Pred. No. 0;		
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Db 36	CCGCTCACATTTGGGATTCGTCAATCTTCTTCTAAACCCGCAAAATTTCTCCATTTCTAC	95		
Qy 61	CAAAATATCCAACTTTTACATTTCTTCTCTGTAATTTATCTGCTCAATCTTTGGTTC	120		
Db 96	CAAAATATCCAACTTTTACTTTCTTCTGTAATTTATCTGCTCAATCTTTGGTTC	155		
Qy 121	CTGACGGAGATGGCGCGATTTTCAGGCATCTCCTCTCGTAGCTTTCAGGATTTTCACGGCCT	180		
Db 156	CTGACGGAGATGGCGCGATTTTCAGGCATCTCCTCTGTAATTTTCACGGCCT	215		
Qy 181	TTGGTTACTCTTCGAGCGCTTCAGACCGCGCTTCGTACAGCTCCTCTCACGATTTGCTT	240		
Db 216	TTGGTTACTCTTCGAGCGCTTCAGACCGCGCTTCGTACAGCTCCTCTCACGATTTGCTT	275		
Qy 241	CATCATCTCCTCTCTCTCTCTGCTCTGCTATTAAAGAAACAATCATCGAGTCCAAGCA	300		
Db 276	CATCATCTCCTCTCTCTCTGCTCTGCTATTAAAGAAACAATCATCGAGTCCAAGCA	335		
Qy 301	ACGATTTTGAAGACGATGAAGAGAAAGTGGTGGAGGAATCGTTTTAAAGCCGAGACT	360		
Db 336	ACGATTTTGAAGACGATGAAGAGAAAGTGGTGGAGGAATCGTTTTAAAGCCGAGACT	395		
Qy 361	TCTACTGGTACAGAACCTTCGAGAGCCAAATATGAGTCTCTTCTTCAACTAGTGTCTTTT	420		
Db 396	TCTACTGGTACAGAACCTTCGAGAGCCAAATATGAGTCTCTTCTTCAACTAGTGTCTTTT	455		
Qy 421	GAGACATGGATCATCAAGCTTCGACGAAGAGTGAATGTTTTCTCTTACAGACTCGGTTAT	480		
Db 456	GAGACATGGATCATCAAGCTTCGACGAAGAGTGAATGTTTTCTCTTACAGACTCGGTTAT	515		



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 QY 181 IMEELGNSWDFRFLAQHIAFYFTMTVFLYILSPRAYHSECVESHAYETYDKFLKA 240
 Db 181 IMEELGNSWDFRFLAQHIAFYFTMTVFLYILSPRAYHSECVESHAYETYDKFLKA 240
 QY 241 SGEELKNMPADIAVKYITGGDLFLDFEQTSTRTNTPRPVLENLYDFVFNIRDDAEHC 300
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 AC Q9ZSQ3;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE IMUTANS (Hypothetical 40.6 kDa protein) (T10114.90)
 DE (AT4G22260/T10114.90)
 GN IM.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, COLUMBIA;
 RA Wu D., Wright D.A., Wetzel C., Voytas D.F., Rodermel S.R.;
 RT "The IMUTANS variegation locus of Arabidopsis defines a mitochondrial
 RT alternative oxidase homologue that functions during early chloroplast
 RT biogenesis.";
 RL Plant Cell 0:0-0(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Liu S.X., Sakano H., Pham P.K., Yamada K., Banh J., Egu P., Lee J.M.,
 RA Toriumi M., Yu G., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "Full length cDNA of gene T10114.90/AT4G22260 (GI:7269072).";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Shinn P., Brooks S., Chao Q., Chen H., Kim C., Ecker J.;
 RT "Full length cDNA sequences of Arabidopsis thaliana.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
 RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RT "Full length cDNA of gene T10114.90/AT4G22260 (GI:7269072).";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Dale J.M., Gibson H.A., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
 RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
 RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
 RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
 RA Davis R.W., Theologis A., Ecker J.R.;
 RT "Arabidopsis cDNA clones.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RL EMBL; AF098072; AAD03599.1; -

DR EMBL; AF326898; AAG41480.1; -
 DR EMBL; AF324563; AAG40014.1; -
 DR EMBL; AF339717; AAK00399.1; -
 DR EMBL; AY045699; AAK74057.1; -
 DR InterPro; IPR002680; AOX.
 DR Pfam; PF01786; AOX; 1.
 KW Hypothetical protein.
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 Best Local Similarity 99.7%; Pred. No. 2.2e-163;
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 Db 241 SGEELKNMPADIAVKYITGGDLFLDFEQTSTRTNTPRPVLENLYDFVFNIRDDAEHC 300
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RESULT 3
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 AC O49631;
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 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Hypothetical 38.7 kDa protein.
 GN T10114.90 OR AT4G22260.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Murphy G., Drost L., Hall C., Hudson S., Ridley P.,
 RA Bancroft I., Mewes H.W., Mayer K., Schueller C.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL021712; CAA16776.1; -
 DR EMBL; AL161557; CAB79181.1; -
 DR InterPro; IPR002680; AOX.
 DR Pfam; PF01786; AOX; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 335 AA; 38674 MW; 3EE8063B73656807 CRC64;
 Query Match 94.3%; Score 1739; DB 10; Length 335;
 Best Local Similarity 95.2%; Pred. No. 6.8e-154;
 Matches 334; Conservative 1; Mismatches 0; Indels 16; Gaps 1;
 QY 1 MAATSGISSGTLTISRPLVTLRRRAAVSYSSSHRLHLPLSSRLLRNHRVQATIL 60

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 20:54:20 ; Search time 3730 Seconds
(without alignments)
10892.096 Million cell updates/sec

Title: US-09-807-867-1
Perfect score: 1396
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2034640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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2: gb.htg.*
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9: gb.pr.*
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12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
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29: em.vi.*
30: em.htg_hum.*
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32: em.htg_other.*
33: em.htg_mus.*
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40: em.htgo_mus.*
41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1320	94.6	1448	8	AF098072	AF098072 Arabidops
3	1302	93.3	1377	8	AF324663	AF324663 Arabidops
4	1302	93.3	1377	8	AY045699	AY045699 Arabidops
5	1302	93.3	1393	8	AF326898	AF326898 Arabidops
6	1054	75.5	1105	8	AF339717	AF339717 Arabidops
7	346	24.8	82891	8	ATT10114	AL021712 Arabidops
8	70	5.0	121	6	AX325051	AX325051 Sequence
9	70	5.0	121	6	AX325052	AX325052 Sequence
10	70	5.0	121	6	AX325055	AX325055 Sequence
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13	70	5.0	121	6	AX325060	AX325060 Sequence
14	70	5.0	121	6	AX325063	AX325063 Sequence
15	70	5.0	121	6	AX325064	AX325064 Sequence
16	70	5.0	121	6	AX325067	AX325067 Sequence
17	70	5.0	121	6	AX325068	AX325068 Sequence
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20	33	2.4	188864	2	AC125664	AC125664 Rattus no
21	32	2.3	581	9	BC020763	BC020763 Homo sapi
22	32	2.3	1499	9	BC017387	BC017387 Homo sapi
23	32	2.3	1920	3	PFGT08	X62393 P. falciparu
24	32	2.3	2267	8	LES306631	AJ308631 Lycopersi
25	32	2.3	2774	8	AF412039	AF412039 Bambusa o
26	32	2.3	20907	2	AC115584	AC115584 Dictyoste
27	32	2.3	160874	2	AC102677	AC102677 Mus muscu
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29	32	2.3	172223	2	AC115985	AC115985 Homo sapi
30	32	2.3	178097	2	AC016704	AC016704 Homo sapi
31	32	2.3	204252	2	AC112392	AC112392 Rattus no
32	32	2.3	206919	2	AC094991	AC094991 Rattus no
33	32	2.3	253136	2	AC095267	AC095267 Rattus no
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35	32	2.3	253305	3	PFMAL3P7	AL034559 Plasmodiu
36	31	2.2	800	9	AB061546	AB061546 Homo sapi
37	31	2.2	921	6	AX364305	AX364305 Sequence
38	31	2.2	982	17	BC017415	BC017415 Homo sapi
39	31	2.2	1247	8	PSPCHS1	X63333 P. sativum P
40	31	2.2	1393	9	BC014380	BC014380 Homo sapi
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42	31	2.2	1560	9	BC019823	BC019823 Homo sapi
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45	31	2.2	2160	9	BC015995	BC015995 Homo sapi

ALIGNMENTS

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DEFINITION 1396 bp mRNA linear PLN 27-NOV-1998
ACCESSION AJ004881
VERSION AJ004881.1 GI:3929646
KEYWORDS Immunans protein.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 1396)
AUTHORS Carol P.
TITLE Direct Submission

Submitted (18-MAR-1998) Carol P., Genetique Molculaire des
Plantes, Universite Joseph Fourier, Cermo, 460 rue de la Piscine,
Saint Martin d'heres, 38053, FRANCE

2 (bases 1 to 1396)

AUTHORS Carol P., Stevenson, D., Kuntz, M., Coupland, G. and Mache, R.

TITLE The immutans locus of arabidopsis encodes a chloroplast alternative
oxidase-like protein involved in phytoene desaturation

JOURNAL Plant Cell

FEATURES

source

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130. .1185

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BASE COUNT 417 a 261 c 294 g 424 t

ORIGIN

Query Match 100.0%; Score 1396; DB 8; Length 1396;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCTCACATTTGGGATTCGTCAATCTTCTCTAAACCCGCAAAATTTCTCATTTCTTAC 60
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Db 1 CCGCTCACATTTGGGATTCGTCAATCTTCTCTAAACCCGCAAAATTTCTCATTTCTTAC 60
|||||

Qy 61 CAAAAATATCCAACTTTTACATTTCTTCTCTGCGAAATATCTGCTCAATCTTTGGTTC 120
|||||
Db 61 CAAAAATATCCAACTTTTACATTTCTTCTCTGCGAAATATCTGCTCAATCTTTGGTTC 120
|||||

Qy 121 CTGACGGAGATGGCGGCGATTTTCAGGCATCTCCTCTGTCAGTTTCAGATTTTCACGGCCT 180
|||||
Db 121 CTGACGGAGATGGCGGCGATTTTCAGGCATCTCCTCTGTCAGTTTCAGATTTTCACGGCCT 180
|||||

Qy 181 TTGGTTACTCTTCGAGCGTCTAGAGCCGCGCTTTTCGTACAGCTCCTCTCACGATTTGCTT 240
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 20:54:20 ; Search time 3730 Seconds
(without alignments)
10892.096 Million cell updates/sec

Title: US-09-807-867-1

Perfect score: 1396

Sequence: 1 ccgtccattgggttcgt.....aaaaaaaaaaaaaaaaaaaa 1396

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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14: gb_vl.*

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38: em_sy.*

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40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	1396	100.0	1396	8	ATJ004881	Arabidops
2	1320	94.6	1448	8	AF098072	Arabidops
3	1302	93.3	1377	8	AF324663	Arabidops
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5	1302	93.3	1393	8	AF326898	Arabidops
6	1054	75.5	1105	8	AF339717	Arabidops
7	346	24.8	82891	8	ATT10114	Arabidops
8	70	5.0	121	6	AX325051	Sequence
9	70	5.0	121	6	AX325052	Sequence
10	70	5.0	121	6	AX325055	Sequence
11	70	5.0	121	6	AX325056	Sequence
12	70	5.0	121	6	AX325059	Sequence
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15	70	5.0	121	6	AX325064	Sequence
16	70	5.0	121	6	AX325067	Sequence
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20	33	2.4	188864	2	AC125664	Rattus no
21	32	2.3	581	9	BC020763	Homo sapi
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23	32	2.3	1920	3	PFGTUB	X62393 P.falci
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25	32	2.3	2774	8	AF412039	Bambusa o
26	32	2.3	20907	2	AC115584	Dictyoste
27	32	2.3	160874	2	AC102677	Mus muscu
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30	32	2.3	178097	2	AC016704	Homo sapi
31	32	2.3	204252	2	AC112392	Rattus no
32	32	2.3	206919	2	AC094991	Rattus no
33	32	2.3	253136	2	AC095267	Rattus no
34	32	2.3	253305	3	PFMAL3P7	Plasmodiu
35	32	2.3	253305	3	PFMAL3P7	Plasmodiu
36	31	2.2	800	9	AB061546	Homo sapi
37	31	2.2	921	6	AX364305	Sequence
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39	31	2.2	1247	8	PSPCHS1	X63333 P.sativu
40	31	2.2	1393	9	BC014380	Homo sapi
41	31	2.2	1447	3	AF262400	Entamoeba
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43	31	2.2	1617	9	AF187859	Homo sapi
44	31	2.2	1848	8	AF012862	Petrossell
45	31	2.2	2160	9	BC015995	Homo sapi

ALIGNMENTS

RESULT 1
ATJ004881
LOCUS
DEFINITION
Arabisopsis thaliana mRNA for Immunans protein.
ACCESSION
AJ004881
VERSION
AJ004881.1 GI:3929646
KEYWORDS
Immunans protein.
SOURCE
thale cress.
ORGANISM
Arabisopsis thaliana
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 1396)
AUTHORS
Carol P.
TITLE
Direct Submission

ATJ004881 1396 bp mRNA linear PLN 27-NOV-1998
Arabisopsis thaliana mRNA for Immunans protein.

REFERENCE 1 (bases 1 to 1448)
 AUTHORS Wu, D., Wright, D.A., Wetzel, C., Voytas, D.F. and Rodermeil, S.R.
 TITLE The IMMUTANS variation locus of Arabidopsis defines a mitochondrial alternative oxidase homologue that functions during early chloroplast biogenesis
 JOURNAL Plant Cell (1999) In press
 AUTHORS 2 (bases 1 to 1448)
 TITLE Direct Submission
 JOURNAL Submitted (09-OCT-1998) Botany, Iowa State University, 463 Bessey Hall, Ames, Iowa 50014, USA
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Query Match 94.6%; Score 1320; DB 8; Length 1448;
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RESULT 3
 AF324663

LOCUS Arabidopsis thaliana AT4g22260 (AT4g22260/T10114_90) mRNA, complete

DEFINITION cds.

ACCESSION AF324663

VERSION AF324663.2

KEYWORDS FLI_CDNA.

SOURCE Arabidopsis thaliana.

ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 1377)
Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Banh, J., Bowser, L.,
Carninci, P., Chung, M.K., Goldsmith, A.D., Hayashizaki, Y., Ishida, J.,
Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M.,
Lin, J., Liu, S.X., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,
Pham, P.K., Quach, H.L., Sakano, H., Sakurai, T., Satou, M., Seki, M.,
Southwick, A., Toriumi, M., Yamada, K., Yu, G., Shinozaki, K.,
Davis, R.W., Theologis, A. and Ecker, J.R.

TITLE

Arabidopsis cDNA clones

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 1377)
Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Banh, J., Bowser, L.,
Carninci, P., Chung, M.K., Goldsmith, A.D., Hayashizaki, Y., Ishida, J.,
Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M.,
Lin, J., Liu, S.X., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,
Pham, P.K., Quach, H.L., Sakano, H., Sakurai, T., Satou, M., Seki, M.,
Southwick, A., Toriumi, M., Yamada, K., Yu, G., Shinozaki, K.,
Davis, R.W., Theologis, A. and Ecker, J.R.

TITLE

Direct Submission

JOURNAL

Submitted (29-NOV-2000) Salk Institute Genomic Analysis Laboratory
(SIGNAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
USA

REFERENCE

3 (bases 1 to 1377)
Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Banh, J., Bowser, L.,
Carninci, P., Chung, M.K., Goldsmith, A.D., Hayashizaki, Y., Ishida, J.,
Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M.,
Lin, J., Liu, S.X., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,
Pham, P.K., Quach, H.L., Sakano, H., Sakurai, T., Satou, M., Seki, M.,
Southwick, A., Toriumi, M., Yamada, K., Yu, G., Shinozaki, K.,
Davis, R.W., Theologis, A. and Ecker, J.R.

TITLE

Direct Submission

JOURNAL

Submitted (09-MAR-2001) Salk Institute Genomic Analysis Laboratory
(SIGNAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
USA

COMMENT

On Mar 9, 2001 this sequence version replaced gi:11692821.
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
Arabidopsis Full-Length cDNA') : Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGECC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Shinn, P., Chen, H.,
Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C., Tracy, S.E., Banh, J.,
Bowser, L., Chung, M.K., Goldsmith, A.D., Jones, T., Karlin-Neumann, G.,
Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M.,
Palm, C.J., Pham, P.K., Quach, H.L., Sakano, H., Southwick, A.,
Tang, C.C., Toriumi, M., Yamada, K., Yu, G., Davis, R.W., Theologis, A.,
and Ecker, J.R.

Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to
this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk)
contributed equally to this work as PIs.

FEATURES

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Matches 1352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 121 ATTTGAGGATCTCTCTGTTGACGATTTACGGGCTTTGGTTACTCTCTGAGAGC 180
QY 199 TCTAGAGCGCGGTTTCTGTTACAGTCTCTCAACGATTTGTTTCTATCTCTCTCTCT 258
Db 181 TCTAGAGCGCGGTTTCTGTTACAGTCTCTCAACGATTTGTTTCTATCTCTCTCTCT 240
QY 259 TCTCTGCTCTGCTATTATGAAGCAATCATCGATTTCAAGCAAGCAAGATTTGCAAGAGAT 318
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Db 361 CTTGAGGAGCAAAATATGAGTTCTTCTCAACTAGTGTCTTGGAGACATGGATCATCAAG 420
QY 439 CTTGAGGAGGAGTGAATGTTTCTTACAGACATCGGTTATTAGATCTGTTGACACTTTG 498
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QY 619 TATTTGAAAGTACACTTTGCTGAGAGCTGGAATGAATGATCATCTGCTCATTAATGAA 678
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RESULT 4			
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DEFINITION	Arabidopsis thaliana AT4g22260/T10114_90 mRNA, complete cds.		
ACCESSION	AY045699		
VERSION	AY045699.1	GI:15010795	
KEYWORDS	FLI CDNA.		
SOURCE	Arabidopsis thaliana.		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
AUTHORS	Kim, C.J., Chen, H., Cheuk, R., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Dale, J.M., Gibson, H.A., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.		
JOURNAL	Arabidopsis cDNA clones		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 1377)		
	Kim, C.J., Chen, H., Cheuk, R., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Dale, J.M., Gibson, H.A., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (06-JUL-2001) Salk Institute Genomic Analysis Laboratory (SIGAL), Plant Biology Laboratory, The Salk Institute for		

Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA') : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Kim, C.J., Chen, H., Cheuk, R., Koesema, E., Meyers, M.C., Shinn, P., Banh, J., Bowser, L., Dale, J.M., Gibson, H.A., Goldsmith, A.D., Jiang, P.X., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.

Kim, C.J. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

FEATURES

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AF339717

LOCUS

DEFINITION

AF339717

VERSION

AF339717.1

KEYWORDS

FLI_CDNA.

SOURCE

Arabidopsis thaliana.

ORGANISM

Arabidopsis thaliana.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 1105)

AUTHORS

Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Etgu, P., Lee, J.M., Toriumi, M., Yu, G., Brooks, S., Chao, Q., Chen, H., Karlin-Neumann, G., Kim, C., Lam, B., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.

TITLE

Arabidopsis Open Reading Frame (ORF) Clones

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 1105)

AUTHORS

Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.

TITLE

Direct Submission

JOURNAL

Submitted (24-JAN-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

COMMENT

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'). Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PCEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B.,

Lin, J., Miranda, M., Nguyen, M., Palm, C. J., Shinn, P., Southwick, A., Davis, R. W., Ecker, J. R. and Theologis, A.

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

FEATURES

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3'UTR

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ORIGIN

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Best Local Similarity 99.9%; Pred. No. 0;

Matches 1104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 7

ATT10114/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

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misc_feature

Location/Qualifiers

organism

variety

db_xref

chromosome

taxon

feature


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DEFINITION Sequence 1189 from Patent WO0192512.
ACCESSION AX325051
VERSION AX325051.1 GI:18095806
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ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1

AUTHORS Kmiec,E.B., Camper,H.B., Rice,M.C. and Kim,J.
TITLE Targeted chromosomal genomic alterations in plants using modified
JOURNAL single stranded oligonucleotides
Patent: WO 0192512-A 1189 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
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Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 143 CAGGCATCTCCTCTGTTGACGTTGACGATTTTCACGGCCTTTTGGTTACTCTTCGACGCTCTA 202
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QY 203 G 203
Db 121 G 121

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LOCUS AX325052 121 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 1190 from Patent WO0192512.
ACCESSION AX325052
VERSION AX325052.1 GI:18095807
KEYWORDS
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1

AUTHORS Kmiec,E.B., Camper,H.B., Rice,M.C. and Kim,J.
TITLE Targeted chromosomal genomic alterations in plants using modified
JOURNAL single stranded oligonucleotides
Patent: WO 0192512-A 1190 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
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QY 143 CAGGCATCTCCTCTGTTGACGTTGACGATTTTCACGGCCTTTTGGTTACTCTTCGACGCTCTA 202
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QY 203 G 203
Db 1 G 1

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LOCUS AX325055 121 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 1193 from Patent WO0192512.
ACCESSION AX325055
VERSION AX325055.1 GI:18095810
KEYWORDS
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
REFERENCE
AUTHORS Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
TITLE Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides
JOURNAL Patent: WO 0192512-A 1193 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
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QY 104 GCTCAATCTTTGGTCTCTGACGGAGATGGCGGCGATTCAGGCATCTCTCTGTAGCT 163
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QY 164 TGACGATTTACGGCTTTGGTTACTCTTCGACGCTCTAGAGCCGCCGTTTCGTACAGCT 223
Db 61 AGAGATTTACGGCTTTGGTTACTCTTCGACGCTCTAGAGCCGCCGTTTCGTACAGCT 120
QY 224 C 224
Db 121 C 121
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DEFINITION Sequence 1194 from Patent WO0192512.
ACCESSION AX325056
VERSION AX325056.1 GI:18095811
KEYWORDS
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
REFERENCE
AUTHORS Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
TITLE Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides
JOURNAL Patent: WO 0192512-A 1194 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
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ACCESSION AX325059
VERSION AX325059.1 GI:18095814
KEYWORDS
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
REFERENCE
AUTHORS Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
TITLE Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides
JOURNAL Patent: WO 0192512-A 1197 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
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LOCUS AX325060/c 121 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 1198 from Patent WO0192512.
ACCESSION AX325060
VERSION AX325060.1 GI:18095815
KEYWORDS
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
REFERENCE
AUTHORS Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
TITLE Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides
JOURNAL Patent: WO 0192512-A 1198 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
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Db 1 G 1

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DEFINITION Sequence 1201 from Patent WO0192512.
ACCESSION AX325063
VERSION AX325063.1 GI:18095818
KEYWORDS
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
1
AUTHORS Kniec,E.B., Gamber,H.B., Rice,M.C. and Kim,J.
TITLE Targeted chromosomal genomic alterations in plants using modified
single stranded oligonucleotides
JOURNAL Patent: WO 0192512-A 1201 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
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Qy 253 C 253
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Db 121 C 121

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DEFINITION Sequence 1202 from Patent WO0192512.
ACCESSION AX325064
VERSION AX325064.1 GI:18095819
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SOURCE thale cress.
ORGANISM Arabidopsis thaliana
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
1
AUTHORS Kniec,E.B., Gamber,H.B., Rice,M.C. and Kim,J.
TITLE Targeted chromosomal genomic alterations in plants using modified
single stranded oligonucleotides
JOURNAL Patent: WO 0192512-A 1201 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
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Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 253 C 253
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Db 121 C 121

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
1
AUTHORS Kniec,E.B., Gamber,H.B., Rice,M.C. and Kim,J.
TITLE Targeted chromosomal genomic alterations in plants using modified
single stranded oligonucleotides
JOURNAL Patent: WO 0192512-A 1202 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Perfect score: 1396
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Gapop 60.0 , Gapext 60.0

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ALIGNMENTS

RESULT 1
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ID AAAL4951 standard; CDNA; 1396 BP.

08-AUG-2000 (first entry)

cdNA of Terminal oxidase associated with biosynthesis of carotenoids.
Terminal oxidase; carotenoid biosynthesis; OPAC; phytoene desaturase;
carotenoid production; fruit colour; tomato; variegated leave;
Vitamin A precursor; beta-carotene; high light intensity; plant injury
ss.

XX
PN
FR2784688-A1.XX
PD 21-APP-2000XX
PF 20-OCT-1998: 98ER-0013283-XX
XX

PR 20-OCT-1998; 98FR-0013283.
XX (UYGR-) UNIV GRENOBLE FOURIER JOSEPH.
XX
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XX Carol S, Kuntz M, Mache R, Coupland G, Stevenson D;
XX WPI; 2000-331435/29.
DR P-PSDB; AAY84869.
XX
XX New DNA encoding terminal oxidase associated with biosynthesis of
PT carotenoids, useful for altering carotenoid content of plants, e.g.
PT changing fruit color -
XX
XX Claim 1; Fig 1; 34pp; French.
XX
XX The present sequence encodes a protein that is a terminal oxidase
CC associated with biosynthesis of carotenoids (OTBC). The polypeptide
CC is associated with carotenoid biosynthesis. The enzyme is found in
CC chloroplast membranes, and is necessary for the function of phytoene
CC desaturase. The OTBC polynucleotide is used to increase carotenoid
CC production in plants, while its complement is used for antisense
CC inhibition of carotenoid biosynthesis, e.g. for modifying the color
CC of fruits such as tomatoes; to generate plants with variegated leaves
CC and to increase the content of the Vitamin A precursor beta-carotene
CC (which is also an anti-oxidant and colorant). Beta-Carotenoids also
CC protect plants against injury caused by high light intensity.
XX
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DB 1381 AAAAAAAAAAAAAAAAAA 1396

RESULT 2

ABN98650/c

ID ABN98650 standard; DNA; 921 BP.

XX AC ABN98650;

XX AC ABN98650;

DT 01-AUG-2002 (first entry)

XX

XX Arabidopsis thaliana expressed polynucleotide SEQ ID NO 418.

XX

XX Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;

KW disease; crop; thale cress; tolerance factor; insect; pathogen;

KW nutrition; ds.

XX

XX Arabidopsis thaliana.

XX

PN US2002023281-A1.
XX 21-FEB-2002.
XX 26-JAN-2001; 2001US-0770445.
XX 27-JAN-2000; 2000US-178472P.
XX (GORL/) GORLACH J.
XX (ANYX/) AN Y.
XX (HAML/) HAMILTON C M.
XX (PRIC/) PRICE J L.
XX (RAIN/) RAINES T M.
XX (YUYX/) YU Y.
XX (RAME/) RAMEAKA J G.
XX (PAGE/) PAGE A.
XX (MATH/) MATHAW A V.
XX (LEDF/) LEDFORD B L.
XX (WOES/) WOESSNER J P.
XX (HAAS/) HAAS W D.
XX (GARC/) GARCIA C A.
XX (KRICK/) KRICKER M.
XX (SLAT/) SLATER T.
XX (DAVI/) DAVIS K R.
XX (ALLE/) ALLEN K.
XX (HOFF/) HOFFMAN N.
XX (HURB/) HURBAN P.
XX Gorrach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
PI Hurban P;
XX WPI: 2002-400781/43.
XX New Arabidopsis thaliana nucleic acid for identifying homologous genes,
PT producing compositions that modulate the expression or function of its
PT encoded protein, and mapping functional regions of protein -
XX Claim 1: SEQ ID NO 418; 49pp + Sequence Listing; English.
XX The invention relates to an Arabidopsis thaliana nucleic acid (I)
CC comprising a sequence capable of hybridising under stringent conditions
CC to a sequence selected from any one of 999 sequences (ABN98233-ABN99231),
CC given in the specification or its fragment. A polypeptide (II) encoded by
CC (I), a transgenic plant (III) comprising an exogenous nucleic acid or a
CC genetically modified cell (IV) comprising an exogenous nucleic acid, is
CC useful for screening a candidate agent for its biological effect. (I) is
CC useful in identifying homologous or related genes, in producing
CC compositions that modulate the expression or function of its encoded
CC protein, mapping functional regions of the protein and in studying
CC associated physiological pathways. (I) is also useful for the genetic
CC manipulation of cells, particularly plant cells. (I) is also useful in
CC screening assays of various plant strains to determine the strains that
CC are best capable of withstanding a particular disease or environmental
CC stress. (II) and (III) are useful for screening of biologically active
CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical
CC pathways. The screened agents are useful in improved methods of treating
CC crops to prevent or treat disease. (II) are also useful in screening
CC programs to identify agents that mimic or enhance the action of tolerance
CC factors. Such agents are useful in improved methods of treating crops to
CC enhance their tolerance to environmental stress. (I) is also useful
CC for enhancing or inhibiting production of a biosynthetic product in a
CC plant. (III) is useful for identifying other mediators that may induce
CC expression of proteins of interest, for establishing the extent to which
CC any specific insect and/or pathogen is responsible for damage to a
CC particular plant, for identifying other mediators that enhance or induce
CC tolerance to environmental stress, for identifying factors involved in
CC biosynthetic pathways of nutritional, commercial, or medicinal value and
CC for identifying productions of nutritional, commercial or medicinal
CC value. (IV) is useful in the study of genetic function and regulation,
CC for alteration of the cellular metabolism and for screening compounds
CC that may affect the biological function of the gene or gene products.

CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocID=999909770445.
XX
SQ Sequence 921 BP; 278 A; 206 C; 153 G; 284 T; 0 other;
Query Match 62.3%; Score 870; DB 24; Length 921;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 920; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 401 CTTCTTCAACTAGTCTTTTGAGACATGGATCATCAAGCTTTGAGCAAGGAGTGAATGTTT 460
DB 921 CTTCTTCAACTAGTCTTTTGAGACATGGATCATCAAGCTTTGAGCAAGGAGTGAATGTTT 862
QY 461 TCCTTACAGACTCGGTATTAAAGATACCTTGACACTTTGTATCGTCGACCAACATATGCAA 520
DB 861 TCCTTACAGACTCGGTATTAAAGATACCTTGACACTTTGTATCGTCGACCAACATATGCAA 802
QY 521 GGTTCCTTTGTTCTTGAGACAATTCGTACAGTCCCTTATTTTGGCGTTTATGTCGTGCTAC 580
DB 801 GGTTCCTTTGTTCTTGAGACAATTCGTACAGTCCCTTATTTTGGCGTTTATGTCGTGCTAC 742
QY 581 ATATGATGAGACCTTTGTTGGTGAGGAGAGCAGATATTTGAAAGATACACTTTGCTG 640
DB 741 ATATGATGAGACCTTTGTTGGTGAGGAGAGCAGATATTTGAAAGATACACTTTGCTG 682
QY 641 AGAGCTGGAATGAATGATCATCATCTTGTCTCAATTAATGGAAGAATTCGGTGGAAATTCCTGGT 700
DB 681 AGAGCTGGAATGAATGATCATCATCTTGTCTCAATTAATGGAAGAATTCGGTGGAAATTCCTGGT 622
QY 701 GGTTCCTTTGTTCTTGAGACAATTCGTACAGTCCCTTATTTTGGCGTTTATGTCGTGCTAC 760
DB 621 GGTTCCTTTGTTCTTGAGACAATTCGTACAGTCCCTTATTTTGGCGTTTATGTCGTGCTAC 562
QY 761 TGTATATCTTAAGCCCTAGATGCGATATCATCTTTTCGGAATGTTGGAGAGTCAATGAT 820
DB 561 TGTATATCTTAAGCCCTAGATGCGATATCATCTTTTCGGAATGTTGGAGAGTCAATGAT 502
QY 821 ATGAGACTTATCATAAATTTCTCAAGGCCAGTGAGAGAGTGAAGAATATGCTCGTGCAC 880
DB 501 ATGAGACTTATCATAAATTTCTCAAGGCCAGTGAGAGAGTGAAGAATATGCTCGTGCAC 442
QY 881 CGGATATCGCAGTAAATTAATCTATACGGGAGTGACTTGTACTTATTTGATGAGTTCCAAA 940
DB 441 CGGATATCGCAGTAAATTAATCTATACGGGAGTGACTTGTACTTATTTGATGAGTTCCAAA 382
QY 941 CATCAAGAACTCCCAATTAATCTATCAAGAACAGTGAATAAGAAAATCTATACGATGTTGTGA 1000
DB 381 CATCAAGAACTCCCAATTAATCTATCAAGAACAGTGAATAAGAAAATCTATACGATGTTGTGA 322
QY 1001 ACATAGAGATGATGAAGCAGAACACTGCAACACATGAGAGCTTGTGAGAGTCTAGGCA 1060
DB 321 ACATAGAGATGATGAAGCAGAACACTGCAACACATGAGAGCTTGTGAGAGTCTAGGCA 262
QY 1061 GTCTCGGTTCTCCACACTCCATTTTATAGATGATGATGATGATGATGATGATGATGATGATG 1120
DB 261 GTCTCGGTTCTCCACACTCCATTTTATAGAGATGATGATGATGATGATGATGATGATGATG 202
QY 1121 TTGTTCTCGAGAGGCTCATTCGGAAGGTATTTGTAGAGTCCCTCAAGAAATCCATACAA 1180
DB 201 TTGTTCTCGAGAGGCTCATTCGGAAGGTATTTGTAGAGTCCCTCAAGAAATCCATACAA 142
QY 1181 GTTAATAAATTAAGAAAGTAAACTAAAAAGATTTATTTGTATCAGCTTCATGAACAATAGAT 1240
DB 141 GTTAATAAATTAAGAAAGTAAACTAAAAAGATTTATTTGTATCAGCTTCATGAACAATAGAT 82
QY 1241 ATAAATCCCATATCTTTGGGAATAAAGGAATAATGTCAAAATTCCTCATGCTGTAGTGT 1300
DB 81 ATAAATCCCATATCTTTGGGAATAAAGGAATAATGTCAAAATTCCTCATGCTGTAGTGT 22
QY 1301 GTGAGAGAAATCAAAATACCCCTA 1321
DB 21 GTGAGAGAAATCAAAATACCCCTA 1

CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance, porphyrin herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention.

XX
SQ Sequence 121 BP; 43 A; 29 C; 29 G; 20 T; 0 other;

Query Match 5.0%; Score 70; DB 24; Length 121;
Best Local Similarity 99.2%; Pred. No. 3.4e-18;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 83 TCTTCTCTGAAATATCTGCTCAAAATCTTGGTTCCTGACGAGATGCGGCGATT 142
DB 121 TCTTCTCTGAAATATCTGCTCAAAATCTTGGTTCCTGACGAGATGCGGCGATT 62
QY 143 CAGGCATCTCTCTGTTAGTTCAGATTTTCACGGCCCTTGGTTACTCTTCGAGGCTCTA 202
DB 61 GAGGCATCTCTCTGTTAGTTCAGATTTTCACGGCCCTTGGTTACTCTTCGAGGCTCTA 2
QY 203 G 203
DB 1 G 1

RESULT 5
ABK25833
ID ABK25833 standard; DNA; 121 BP.
AC ABK25833;
DT 09-APR-2002 (first entry)
DE Albino plant producing genome altering oligonucleotide #5.

KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KW porphyrin herbicide resistance; triazine resistance; disease resistance;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.

XX Arabidopsis thaliana.
OS Synthetic.
PN WO200192512-A2.
XX
XX 06-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-US17672.
XX
PR 01-JUN-2000; 2000US-208538P.
PR 30-OCT-2000; 2000US-244989P.
PR 27-MAR-2001; 2001US-0818875.

XX
PA (UYDE) UNIV DELAWARE.
XX Kmiec EB, Gamber HB, Rice MC, Kim J;
XX WPI; 2002-106307/14.
XX
XX New oligonucleotides with modified nuclease-resistant termini, useful
XX for creating plants with desired phenotypes, e.g. stress tolerance,
XX improved nutritional value, herbicide or disease resistance, or
XX modified oil production -
XX
XX Claim 7: Page 115; 220pp: English.
XX
XX The invention relates to an oligonucleotide for targeted alteration of a
XX genetic sequence, which comprises a single-stranded oligonucleotide
XX having a DNA domain. The DNA domain has at least one mismatch with
XX respect to the genetic sequence to be altered and further comprises
XX chemical modifications of the oligonucleotide. The chemical modifications
XX consist of o-methyl modification, an LNA modification, two or more
XX phosphorothioate linkages on a terminus, or a combination of any two or
XX more of these modifications. The oligonucleotides are useful for
XX directing repair or alteration of plant genetic information. The
XX oligonucleotides are particularly useful for creating plants with desired
XX phenotypes, e.g. environmental or abiotic stress tolerance, improved
XX nutritional value (e.g. altering amino acid content of plants or
XX conferring amino acid over production), herbicide resistance (e.g.
XX glyphosate resistance, imidazolinone and sulphonylurea herbicide
XX resistance, porphyrin herbicide resistance or triazine resistance),
XX disease resistance, modified oil production, modified starch production
XX (e.g. increased starch or production of waxy starch), altered floral
XX morphology (e.g. male-sterile plants) or modified fatty acid content
XX (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
XX The oligonucleotides are also useful for producing albino mutants for the
XX analysis of photosynthetic processes. This sequence represents a genome
XX altering oligonucleotide of the invention.

XX
SQ Sequence 121 BP; 20 A; 34 C; 31 G; 36 T; 0 other;

Query Match 5.0%; Score 70; DB 24; Length 121;
Best Local Similarity 99.2%; Pred. No. 3.4e-18;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 104 GCTCAAAATCTTGGTTCCTGACGAGATGCGGCGATTTCAGGCATCTCTCTGTTACGT 163
DB 1 GCTCAAAATCTTGGTTCCTGACGAGATGCGGCGATTTCAGGCATCTCTCTGTTACGT 60
QY 164 TGACGATTTTCAGGCCTTTGGTTACTCTTCAGGCTCTAGAGCCGCGTTTCGTACAGCT 223
DB 61 AGACGATTTTCAGGCCTTTGGTTACTCTTCAGGCTCTAGAGCCGCGTTTCGTACAGCT 120
QY 224 C 224
DB 121 C 121

RESULT 6
ABK25834/c
ID ABK25834 standard; DNA; 121 BP.
XX ABK25834;
XX
XX 09-APR-2002 (first entry)
XX
XX Albino plant producing genome altering oligonucleotide #6.
XX
XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KW porphyrin herbicide resistance; triazine resistance; disease resistance;

modified oil production; modified starch production; waxy starch;
 altered floral morphology; male-sterile plant; albino mutant;
 modified fatty acid content; reduced palmitate production; albino plant;
 increased stearate production; reduced linolenic acid production;
 photosynthetic process.

KW Arabidopsis thaliana.
 OS Synthetic.
 OS WO200192512-A2.
 XX 06-DEC-2001.
 XX 01-JUN-2001; 2001WO-US17672.
 XX 01-JUN-2000; 2000US-208538P.
 PR 30-OCT-2000; 2000US-244989P.
 PR 27-MAR-2001; 2001US-0818875.
 XX (UYDE) UNIV DELAWARE.
 PA Kmiec EB, Gamper HB, Rice MC, Kim J;
 PI WPI; 2002-106307/14.
 DR New oligonucleotides with modified nuclease-resistant termini, useful
 for creating plants with desired phenotypes, e.g. stress tolerance,
 improved nutritional value, herbicide or disease resistance, or
 modified oil production -
 XX Claim 7; Page 115; 220pp; English.
 PS The invention relates to an oligonucleotide for targeted alteration of a
 CC genetic sequence, which comprises a single-stranded oligonucleotide
 CC having a DNA domain. The DNA domain has at least one mismatch with
 CC respect to the genetic sequence to be altered and further comprises
 CC chemical modifications of the oligonucleotide. The chemical modifications
 CC consist of o-methyl modification, an LNA modification, two or more
 CC phosphorothioate linkages on a terminus, or a combination of any two or
 CC more of these modifications. The oligonucleotides are useful for
 CC directing repair or alteration of plant genetic information. The
 CC oligonucleotides are particularly useful for creating plants with desired
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
 CC nutritional value (e.g. altering amino acid content of plants or
 CC conferring amino acid over production), herbicide resistance (e.g.
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
 CC resistance, porphyrin herbicide resistance or triazine resistance),
 CC disease resistance, modified oil production, modified starch production
 CC (e.g. increased starch or production of waxy starch), altered floral
 CC morphology (e.g. male-sterile plants) or modified fatty acid content
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
 CC The oligonucleotides are also useful for producing albino mutants for the
 CC analysis of photosynthetic processes. This sequence represents a genome
 CC altering oligonucleotide of the invention.
 XX Sequence 121 BP; 36 A; 31 C; 34 G; 20 T; 0 other;
 SQ
 Query Match 5.0%; Score 70; DB 24; Length 121;
 Best Local Similarity 99.2%; Pred. No. 3.4e-18;
 Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 104 GCTCAATCTTGGTTCCTGACGGAGATGGCGGCGATTTCAGGCATCTCCTGTGACGT 163
 Db |||||||
 121 GCTCAATCTTGGTTCCTGACGGAGATGGCGGCGATTTCAGGCATCTCCTGTGACGT 62
 QY 164 TGACGATTTACCGCGCTTTGGTTACTCTTCGACGCTCTAGAGCCGCGTTTCGTACAGCT 223
 Db |||||||
 61 AGACGATTTACCGCGCTTTGGTTACTCTTCGACGCTCTAGAGCCGCGTTTCGTACAGCT 2
 QY 224 C 224
 Db |
 1 C 1

RESULT 7
 ABK25837
 ID ABK25837 standard; DNA; 121 BP.
 XX AC ABK25837;
 XX 09-APR-2002 (first entry)
 XX Albino plant producing genome altering oligonucleotide #9.
 KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
 KW o-methyl modification; LNA modification; phosphorothioate linkage;
 KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
 KW abiotic stress tolerance; improved nutritional value; hygromycin-B;
 KW amino acid over production; herbicide resistance; glyphosate resistance;
 KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
 KW porphyrin herbicide resistance; triazine resistance; disease resistance;
 KW modified oil production; modified starch production; waxy starch;
 KW altered floral morphology; male-sterile plant; albino mutant;
 KW modified fatty acid content; reduced palmitate production; albino plant;
 KW increased stearate production; reduced linolenic acid production;
 KW photosynthetic process.
 OS Arabidopsis thaliana.
 OS Synthetic.
 PN WO200192512-A2.
 XX 06-DEC-2001.
 XX 01-JUN-2001; 2001WO-US17672.
 XX 01-JUN-2000; 2000US-208538P.
 PR 30-OCT-2000; 2000US-244989P.
 PR 27-MAR-2001; 2001US-0818875.
 XX (UYDE) UNIV DELAWARE.
 PA Kmiec EB, Gamper HB, Rice MC, Kim J;
 PI WPI; 2002-106307/14.
 DR New oligonucleotides with modified nuclease-resistant termini, useful
 for creating plants with desired phenotypes, e.g. stress tolerance,
 improved nutritional value, herbicide or disease resistance, or
 modified oil production -
 XX Claim 7; Page 115; 220pp; English.
 PS The invention relates to an oligonucleotide for targeted alteration of a
 CC genetic sequence, which comprises a single-stranded oligonucleotide
 CC having a DNA domain. The DNA domain has at least one mismatch with
 CC respect to the genetic sequence to be altered and further comprises
 CC chemical modifications of the oligonucleotide. The chemical modifications
 CC consist of o-methyl modification, an LNA modification, two or more
 CC phosphorothioate linkages on a terminus, or a combination of any two or
 CC more of these modifications. The oligonucleotides are useful for
 CC directing repair or alteration of plant genetic information. The
 CC oligonucleotides are particularly useful for creating plants with desired
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
 CC nutritional value (e.g. altering amino acid content of plants or
 CC conferring amino acid over production), herbicide resistance (e.g.
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
 CC resistance, porphyrin herbicide resistance or triazine resistance),
 CC disease resistance, modified oil production, modified starch production
 CC (e.g. increased starch or production of waxy starch), altered floral
 CC morphology (e.g. male-sterile plants) or modified fatty acid content
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
 CC The oligonucleotides are also useful for producing albino mutants for the
 CC analysis of photosynthetic processes. This sequence represents a genome
 CC altering oligonucleotide of the invention.
 XX

```
SQ Sequence 121 BP; 17 A; 35 C; 32 G; 37 T; 0 other;
Query Match 5.0%; Score 70; DB 24; Length 121;
Best Local Similarity 99.2%; Pred. No. 3.4e-18;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 113 TTTGGTTCTGACGAGATGGCGGATTCAGGCACTCTCTGGTACGTTGACGATTT 172
Db 1 TTTGGTTCTGACGAGATGGCGGATTCAGGCACTCTCTGGTACGTTGACGATTT 60

QY 173 CACGGCTTTGGTTACTCTTCGACGCTCTAGAGCGCGCTTTCGTACAGCTCTCTCAAC 232
Db 61 GACGGCTTTGGTTACTCTTCGACGCTCTAGAGCGCGCTTTCGTACAGCTCTCTCAAC 120

QY 233 G 233
Db 121 G 121

RESULT 8
ABK25838/c
ID ABK25838 standard; DNA; 121 BP.
XX
AC ABK25838;
XX
DT 09-APR-2002 (first entry)
XX
DE Albino plant producing genome altering oligonucleotide #10.
XX
KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; triazine resistance; disease resistance;
KW porphyrin herbicide resistance; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.
XX
OS Arabidopsis thaliana.
OS Synthetic.
XX
PN WO200192512-A2.
XX
PD 06-DEC-2001.
XX
PP 01-JUN-2001; 2001WO-US17672.
XX
PR 01-JUN-2000; 2000US-208538P.
PR 30-OCT-2000; 2000US-244989P.
XX 27-MAR-2001; 2001US-0818875.
XX
PA (UYDE ) UNIV DELAWARE.
XX
XX Kmiec EB, Gamper HB, Rice MC, Kim J;
XX WPI; 2002-106307/14.
XX
DR New oligonucleotides with modified nuclease-resistant termini, useful
PT for creating plants with desired phenotypes, e.g. stress tolerance,
PT improved nutritional value, herbicide or disease resistance, or
PT modified oil production
XX
PS Claim 7; Page 115; 220pp; English.
XX
CC The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
```

```
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance, porphyrin herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention.
XX
SQ Sequence 121 BP; 37 A; 32 C; 35 G; 17 T; 0 other;
Query Match 5.0%; Score 70; DB 24; Length 121;
Best Local Similarity 99.2%; Pred. No. 3.4e-18;
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QY 113 TTTGGTTCTGACGAGATGGCGGATTCAGGCACTCTCTGGTACGTTGACGATTT 172
Db 121 TTTGGTTCTGACGAGATGGCGGATTCAGGCACTCTCTGGTACGTTGACGATTT 62

QY 173 CACGGCTTTGGTTACTCTTCGACGCTCTAGAGCGCGCTTTCGTACAGCTCTCTCAAC 232
Db 61 GACGGCTTTGGTTACTCTTCGACGCTCTAGAGCGCGCTTTCGTACAGCTCTCTCAAC 2

QY 233 G 233
Db 1 G 1

RESULT 9
ABK25841
ID ABK25841 standard; DNA; 121 BP.
XX
AC ABK25841;
XX
DT 09-APR-2002 (first entry)
XX
DE Albino plant producing genome altering oligonucleotide #13.
XX
KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; triazine resistance; disease resistance;
KW porphyrin herbicide resistance; modified starch production; waxy starch;
KW modified oil production; modified starch production; disease resistance;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.
XX
OS Arabidopsis thaliana.
OS Synthetic.
XX
PN WO200192512-A2.
XX
PD 06-DEC-2001.
XX
PP 01-JUN-2001; 2001WO-US17672.
XX
PR 01-JUN-2000; 2000US-208538P.
PR 30-OCT-2000; 2000US-244989P.
XX 27-MAR-2001; 2001US-0818875.
XX
```

PA (UYDE) UNIV DELAWARE.
XX
XX Kmiec EB, Gamper HB, Rice MC, Kim J;
XX WPI; 2002-106307/14.
XX
XX New oligonucleotides with modified nuclease-resistant termini, useful
PT for creating plants with desired phenotypes, e.g. stress tolerance,
PT improved nutritional value, herbicide or disease resistance, or
PT modified oil production -
XX
XX Claim 7; Page 115; 220pp; English.
XX
XX The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance, porphyrin herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention.
XX
SQ Sequence 121 BP; 17 A; 39 C; 25 G; 40 T; 0 other;

Query Match 5.0%; Score 70; DB 24; Length 121;
Best Local Similarity 99.2%; Pred. No. 3.4e-18;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 133 GCGGCGATTTCAGGCATCTCTCTGTCAGCTTCACGATTTCACGGCTTTGGTACTCTT 192
DB 1 GCGGCGATTTCAGGCATCTCTCTGTCAGCTTCACGATTTCACGGCTTTGGTACTCTT 60

QY 193 CGAGCTCTAGAGCCGCGCTTTCGTACAGCTCTCTACCGATTGCTTCATCATCTTCT 252
DB 61 TGACGCTCTAGAGCCGCGCTTTCGTACAGCTCTCTACCGATTGCTTCATCATCTTCT 120

QY 253 C 253
DB 121 C 121

RESULT 10
ABK25842/c
ID ABK25842 standard; DNA; 121 BP.
XX
XX AC ABK25842;
XX
XX 09-APR-2002 (first entry)
XX
XX Albino plant producing genome altering oligonucleotide #14.
XX
XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KW porphyrin herbicide resistance; triazine resistance; disease resistance;
KW modified oil production; modified starch production; waxy starch;

KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.
XX
XX Arabidopsis thaliana.
OS Synthetic.
XX
XX WO200192512-A2.
XX
XX PD 06-DEC-2001.
XX
XX 01-JUN-2001; 2001WO-US17672.
XX
XX 01-JUN-2000; 2000US-208538P.
PR 30-OCT-2000; 2000US-244989P.
XX 27-MAR-2001; 2001US-0818875.
XX
XX (UYDE) UNIV DELAWARE.
XX
XX Kmiec EB, Gamper HB, Rice MC, Kim J;
XX
XX WPI; 2002-106307/14.
XX
XX New oligonucleotides with modified nuclease-resistant termini, useful
PT for creating plants with desired phenotypes, e.g. stress tolerance,
PT improved nutritional value, herbicide or disease resistance, or
PT modified oil production -
XX
XX Claim 7; Page 115; 220pp; English.
XX
XX The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance, porphyrin herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention.
XX
SQ Sequence 121 BP; 40 A; 25 C; 39 G; 17 T; 0 other;

Query Match 5.0%; Score 70; DB 24; Length 121;
Best Local Similarity 99.2%; Pred. No. 3.4e-18;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 133 GCGGCGATTTCAGGCATCTCTCTGTCAGCTTCACGATTTCACGGCTTTGGTACTCTT 192
DB 121 GCGGCGATTTCAGGCATCTCTCTGTCAGCTTCACGATTTCACGGCTTTGGTACTCTT 62

QY 193 CGAGCTCTAGAGCCGCGCTTTCGTACAGCTCTCTACCGATTGCTTCATCATCTTCT 252
DB 61 TGACGCTCTAGAGCCGCGCTTTCGTACAGCTCTCTACCGATTGCTTCATCATCTTCT 2

QY 253 C 253
DB 1 C 1

RESULT 11
ABK25845
ID ABK25845 standard; DNA: 121 BP.
XX
AC ABK25845;
XX
DT 09-APR-2002 (first entry)
XX
DE Albino plant producing genome altering oligonucleotide #17.
XX
KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin-B;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; triazine resistance; disease resistance;
KW porphyrin herbicide resistance; modified starch production; waxy starch;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.
XX
OS Arabidopsis thaliana.
OS Synthetic.
XX
PN WO200192512-A2.
XX
PD 06-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-US17672.
XX
PR 01-JUN-2000; 2000US-208538P.
PR 30-OCT-2000; 2000US-244989P.
PR 27-MAR-2001; 2001US-0818875.
XX
PA (UYDE) UNIV DELAWARE.
XX
PI Kmiec EB, Gamper HB, Rice MC, Kim J;
XX WPI; 2002-106307/14.
XX
XX New oligonucleotides with modified nuclease-resistant termini, useful
PT for creating plants with desired phenotypes, e.g. stress tolerance,
PT improved nutritional value, herbicide or disease resistance, or
PT modified oil production -
XX
PS Claim 7; Page 116; 220pp; English.
XX
CC The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance, porphyrin herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention.
XX
SQ Sequence 121 BP; 15 A; 42 C; 21 G; 43 T; 0 other;

Query Match 5.0%; Score 70; DB 24; Length 121;
Best Local Similarity 99.2%; Pred No. 3.4e-18;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 142 TCAGGCATCTCCTCTGCTAGCTTACAGGATTCACGGCCCTTGGTTACTCTTCGAGCTCT 201
DB 1 TCAGGCATCTCCTCTGCTAGCTTACAGGATTCACGGCCCTTGGTTACTCTTCGAGCTCT 60
QY 202 AGAGCCGCCGTTTCGTACAGCTCCTCTACAGGATTCACGGATTCCTCTCTCTCTCTCTCT 261
DB 61 TGAGCCGCCGTTTCGTACAGCTCCTCTACAGGATTCCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 262 C 262
DB 121 C 121
RESULT 12
ABK25846/C
ID ABK25846 standard; DNA: 121 BP.
XX
AC ABK25846;
XX
DT 09-APR-2002 (first entry)
XX
DE Albino plant producing genome altering oligonucleotide #18.
XX
KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin-B;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; triazine resistance; disease resistance;
KW porphyrin herbicide resistance; modified starch production; waxy starch;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.
XX
OS Arabidopsis thaliana.
OS Synthetic.
XX
PN WO200192512-A2.
XX
PD 06-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-US17672.
XX
PR 01-JUN-2000; 2000US-208538P.
PR 30-OCT-2000; 2000US-244989P.
PR 27-MAR-2001; 2001US-0818875.
XX
PA (UYDE) UNIV DELAWARE.
XX
PI Kmiec EB, Gamper HB, Rice MC, Kim J;
XX WPI; 2002-106307/14.
XX
XX New oligonucleotides with modified nuclease-resistant termini, useful
PT for creating plants with desired phenotypes, e.g. stress tolerance,
PT improved nutritional value, herbicide or disease resistance, or
PT modified oil production -
XX
PS Claim 7; Page 116; 220pp; English.
XX
CC The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance, porphyrin herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention.
XX
SQ Sequence 121 BP; 15 A; 42 C; 21 G; 43 T; 0 other;

phosphorothioate linkages on a terminus, or a combination of any two or more of these modifications. The oligonucleotides are useful for directing repair or alteration of plant genetic information. The oligonucleotides are particularly useful for creating plants with desired phenotypes, e.g. environmental or abiotic stress tolerance, improved nutritional value (e.g. altering amino acid content of plants or conferring amino acid over production), herbicide resistance (e.g. glyphosate resistance, imidazolinone and sulphonylurea herbicide resistance, porphyrin herbicide resistance or triazine resistance), disease resistance, modified oil production, modified starch production (e.g. increased starch or production of waxy starch), altered floral morphology (e.g. male-sterile plants) or modified fatty acid content (e.g. reduced palmitate, increased stearate or reduced linolenic acid). The oligonucleotides are also useful for producing albino mutants for the analysis of photosynthetic processes. This sequence represents a genome altering oligonucleotide of the invention.

Sequence 121 BP; 43 A; 21 C; 42 G; 15 T; 0 other;

Query Match 5.0%; Score 70; DB 24; Length 121;
Best Local Similarity 99.2%; Pred. No. 3.4e-18;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 142 TCAGGCATCTCTCTGTTACGATTTCACGGCCTTGGTTACTCTTCGACGCTCT 201
Db |
121 TCAGGCATCTCTCTGTTACGATTTCACGGCCTTGGTTACTCTTCGACGCTCT 62
QY 202 AGACGCCCGCTTTCGTACAGCTCTCTCACCGATTGCTTCATCATCTCTCTCTCTCT 261
Db |
61 TGACGCCCGCTTTCGTACAGCTCTCTCACCGATTGCTTCATCATCTCTCTCTCTCT 2

QY 262 C 262

Db 1 C 1

RESULT 13

ABV37004/C
ID ABV37004 standard; cDNA; 401 BP.

AC ABV37004;

16-SEP-2002 (first entry)

Human prostate expression marker cDNA 36995.

Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
pharmacogenomic marker; gene; ss.

Homo sapiens.

WO200160860-A2.

23-AUG-2001.

20-FEB-2001; 2001WO-US05171.

17-FEB-2000; 2000US-183319P.

16-MAR-2000; 2000US-189862P.

25-MAY-2000; 2000US-207454P.

09-JUN-2000; 2000US-211314P.

18-JUL-2000; 2000US-219007P.

13-DEC-2000; 2000US-255281P.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Schlegel R, Endege WO, Monahan JE;

WPI; 2001-662795/76.

Novel isolated nucleic acid molecule associated with cancerous state of

prostate cells and correlating with presence of prostate cancer, useful

for detecting presence of prostate cancer, stage of prostate cancer -

XX

PS Claim 1; Page 7618; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

Sequence 401 BP; 96 A; 73 C; 84 G; 148 T; 0 other;

Query Match 2.4%; Score 34; DB 23; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.00053;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1363 CATTTTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1396

Db |

95 CATTTTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 62

RESULT 14

ABV07791

ID ABV07791 standard; cDNA; 328 BP.

AC ABV07791;

13-SEP-2002 (first entry)

Human prostate expression marker cDNA 7782.

Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
pharmacogenomic marker; gene; ss.

Homo sapiens.

WO200160860-A2.

23-AUG-2001.

20-FEB-2001; 2001WO-US05171.

17-FEB-2000; 2000US-183319P.

16-MAR-2000; 2000US-189862P.

25-MAY-2000; 2000US-207454P.

09-JUN-2000; 2000US-211314P.

18-JUL-2000; 2000US-219007P.

13-DEC-2000; 2000US-255281P.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Schlegel R, Endege WO, Monahan JE;

WPI; 2001-662795/76.

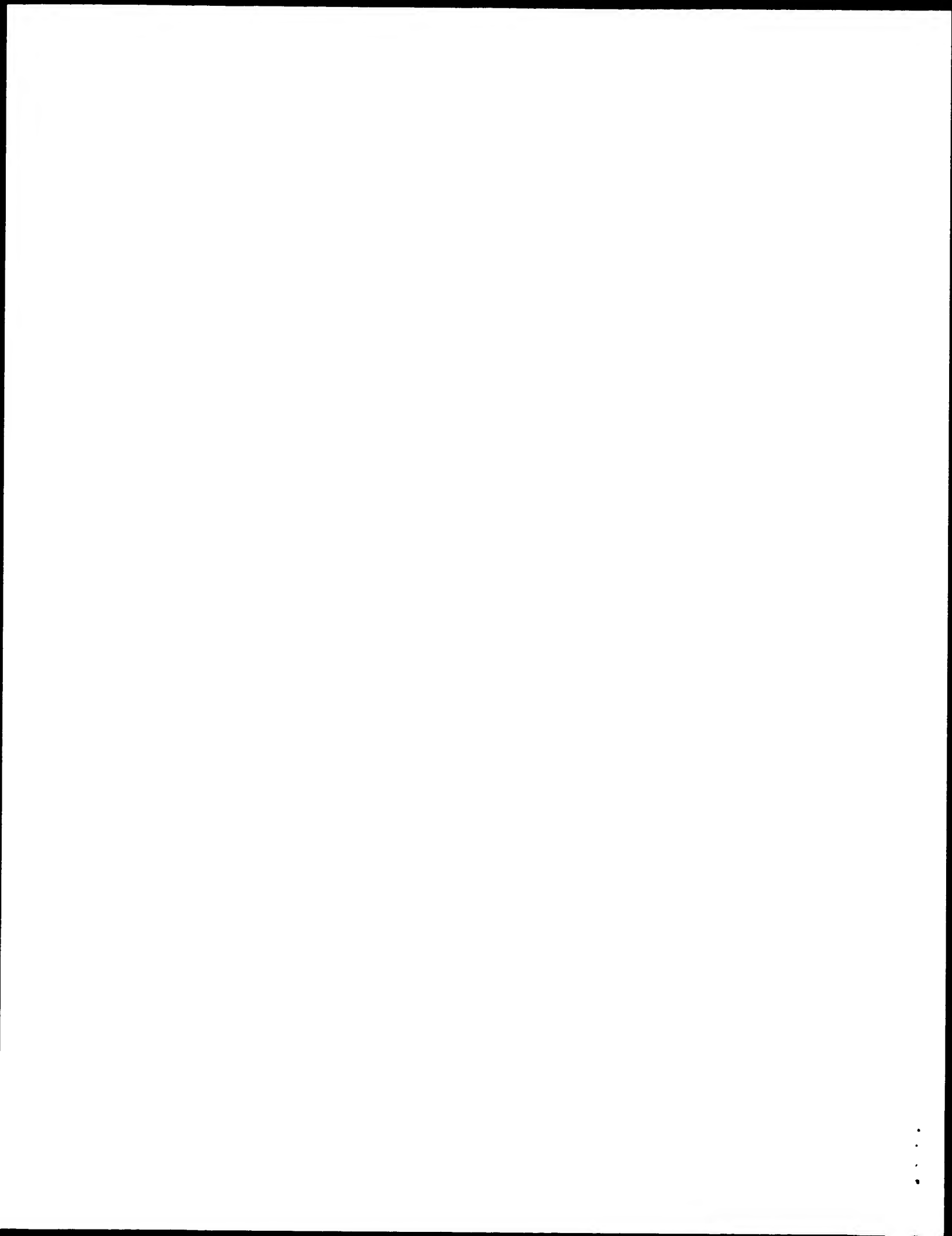
Novel isolated nucleic acid molecule associated with cancerous state of
prostate cells and correlating with presence of prostate cancer, useful
for detecting presence of prostate cancer, stage of prostate cancer -

Claim 1; Page 1249; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 328 BP; 139 A; 52 C; 48 G; 88 T; 1 other;
 Query Match 2.4%; Score 33; DB 23; Length 328;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1364 ATTTTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
 Db 170 ATTTTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 202
 RESULT 15
 AAH87785/C
 ID AAH87785 standard; cDNA; 574 BP.
 XX
 AC AAH87785;
 DT 25-SEP-2001 (first entry)
 XX
 DE Peppermint plant oil gland expressed cDNA 141.
 XX
 KW Peppermint; plant oil gland cell; terpenoid essential oil; resin;
 KW genetic mapping; antisense suppression; recombinant expression; ss.
 XX
 OS Mentha x piperita.
 XX
 PN WO200153319-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 19-JAN-2001; 2001WO-US02567.
 XX
 PR 20-JAN-2000; 2000US-0177264.
 XX
 PA (CROT/) CROTEAU R B.
 PA (LANG/) LANGE B M.
 PA (WILD/) WILDUNG M R.
 XX
 PI Croteau RB, Lange BM, Wildung MR;
 XX
 DR WPI; 2001-488706/53.
 XX
 PT New nucleic acid molecules corresponding to mRNA molecules expressed in
 PT peppermint oil glands for enhancing expression of plant oil gland cell
 PT proteins -
 XX
 PS Claim 1; Page 131; 251pp; English.
 XX
 CC The invention relates to nucleic acid molecules (AAH87645-AAH88116) that
 CC correspond to all or part of a mRNA molecule expressed in plant oil
 CC gland cells, especially peppermint and plant oil glands that produce
 CC terpenoid essential oils and resins. The nucleic acids are useful for
 CC genetically mapping a plant genome for genes expressed in plant oil
 CC gland cells and to suppress (for example by antisense suppression) or
 CC enhance their expression (for example by genetically transforming a
 CC plant cell with a replicable expression vector that expresses one or more
 CC proteins naturally expressed in plant oil gland cells). The nucleic acids
 CC are also useful for recombinant expression of plant oil gland proteins
 CC required for terpenoid essential oil and/or resin production in bacterial
 CC and/or yeast cells.

XX
 SQ Sequence 574 BP; 177 A; 137 C; 113 G; 147 T; 0 other;
 Query Match 2.3%; Score 32; DB 22; Length 574;
 Best Local Similarity 100.0%; Pred. No. 0.0031;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1364 ATTTTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1395
 Db 32 ATTTTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
 Search completed: February 2, 2003, 21:01:19
 Job time : 329 secs



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 20:07:44 : Search time 65 Seconds
(without alignments)
6586.473 Million cell updates/sec

Title: US-09-807-867-1
Perfect score: 1396
Sequence: 1 ccgcacattggattcgt.....aaaaaaaaaaaaaaaaaaaaa 1396

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	33	2.4	1739	4 US-09-594-193-1	Sequence 1, Appli
2	31	2.2	1617	4 US-09-444-336-4	Sequence 4, Appli
3	31	2.2	4337	3 US-09-187-049-1	Sequence 1, Appli
4	30	2.1	1255	4 US-09-149-476-75	Sequence 75, Appli
5	30	2.1	1448	4 US-09-387-212-12	Sequence 12, Appli
6	30	2.1	1448	4 US-09-948-802-12	Sequence 12, Appli
7	30	2.1	1622	4 US-09-334-601-9	Sequence 9, Appli
8	30	2.1	1889	3 US-08-861-747-3	Sequence 3, Appli
9	29	2.1	732	4 US-09-149-476-66	Sequence 66, Appli
10	29	2.1	1012	4 US-09-615-192A-94	Sequence 94, Appli
11	29	2.1	1026	2 US-08-713-000-6	Sequence 6, Appli
12	29	2.1	1026	2 US-08-975-316-6	Sequence 6, Appli
13	29	2.1	1026	4 US-09-211-710-6	Sequence 6, Appli
14	29	2.1	1026	4 US-09-615-192A-6	Sequence 6, Appli
15	29	2.1	1066	2 US-08-605-106-3	Sequence 3, Appli
16	29	2.1	1318	4 US-09-443-041A-25	Sequence 25, Appli
17	28	2.0	945	4 US-09-268-364-3	Sequence 3, Appli
18	28	2.0	1001	1 US-08-728-259A-10	Sequence 10, Appli
19	28	2.0	1001	2 US-08-473-486-10	Sequence 10, Appli
20	28	2.0	1098	3 US-09-248-335-35	Sequence 35, Appli
21	28	2.0	1275	3 US-08-725-532A-2	Sequence 2, Appli
22	28	2.0	1587	3 US-09-108-020-11	Sequence 11, Appli
23	28	2.0	1737	4 US-09-416-050A-7	Sequence 7, Appli
24	28	2.0	1737	4 US-09-664-800-7	Sequence 7, Appli
25	28	2.0	1737	4 US-09-665-309-7	Sequence 7, Appli
26	28	2.0	1737	4 US-09-661-569-7	Sequence 7, Appli
27	28	2.0	1957	4 US-09-352-990-11	Sequence 11, Appli

28 28 2.0 2017 4 US-09-291-922-21 Sequence 21, Appli
29 28 2.0 2158 1 US-07-602-608-1 Sequence 1, Appli
30 28 2.0 2158 1 US-08-261-578-1 Sequence 1, Appli
31 28 2.0 2606 4 US-09-234-827B-3 Sequence 3, Appli
32 28 2.0 4032 1 US-08-126-587C-8 Sequence 8, Appli
33 28 2.0 59065 4 US-09-813-817-3 Sequence 3, Appli
34 28 2.0 59065 4 US-09-978-197-3 Sequence 3, Appli
35 27 1.9 42 1 US-08-741-881-3 Sequence 3, Appli
36 27 1.9 42 1 US-08-739-158-3 Sequence 3, Appli
37 27 1.9 42 2 US-08-739-167-3 Sequence 3, Appli
38 27 1.9 42 3 US-08-404-796-3 Sequence 3, Appli
39 27 1.9 42 3 US-08-931-869-3 Sequence 3, Appli
40 27 1.9 42 4 US-09-350-399-3 Sequence 3, Appli
41 27 1.9 42 4 US-09-236-140A-3 Sequence 3, Appli
42 27 1.9 48 1 US-08-741-881-21 Sequence 21, Appli
43 27 1.9 48 1 US-08-739-158-21 Sequence 21, Appli
44 27 1.9 48 2 US-08-739-167-21 Sequence 21, Appli
45 27 1.9 48 3 US-08-404-796-21 Sequence 21, Appli

ALIGNMENTS

RESULT 1
US-09-594-193-1
; Sequence 1, Application US/09594193
; Patent No. 6441274
; GENERAL INFORMATION:
; APPLICANT: CAHOON, REBECCA E.
; APPLICANT: LOHMAN, KARIN
; TITLE OF INVENTION: NOVEL PLANT TRYPTOPHAN SYNTHASE BETA SUBUNIT
; FILE REFERENCE: B1374 US NA
; CURRENT APPLICATION NUMBER: US/09/594,193
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,568
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1739
; TYPE: DNA
; ORGANISM: Zea mays
US-09-594-193-1

Query Match 2.4% Score 33; DB 4; Length 1739;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1364 ATTTTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
|||||
Db 1701 ATTTTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1733

RESULT 2
US-09-444-336-4
; Sequence 4, Application US/09444336
; Patent No. 6410713
; GENERAL INFORMATION:
; APPLICANT: Guerriero, Vincent
; APPLICANT: Raynes, Deborah A
; TITLE OF INVENTION: DNA Encoding Proteins That Inhibit Hsp70 Function
; FILE REFERENCE: HspBP DNA and Protein Sequences
; CURRENT APPLICATION NUMBER: US/09/444,336
; CURRENT FILING DATE: 1999-11-19
; EARLIER APPLICATION NUMBER: 60/109,351
; EARLIER FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1617
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-444-336-4

Query Match 2.2%; Score 31; DB 4; Length 1617;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 31; Conservative 0; Mismatches 0 Indels

Qy	1366	TTTATCAAAAAAAAAAAAAAAAAA	1396
Db	1587	TTTATCAAAAAAAAAAAAAAAAAA	1617

RESULT 3

US-09-187-049-1
; Sequence 1, Application US/09187049

Patent No. 6117666
GENERAL INFORMATION:
APPLICANT: Lamda, Gayle K.
TITLE OF INVENTION: PLASTID PROTEOLYTIC PROCESSING ENZYME
TITLE OF INVENTION: THAT CLEAVES PRECURSOR POLYPEPTIDES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS HOFER GILSON & LIONE
STREET: P.O. Box 10395

Query Match 2.2%; Score 31; DB 3; Length 4337;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 31; Conservative 0; Mismatches 0; Indels

2y	1366	TTTATCAAAAAAAAAAAAAAAAAA	1396
db	4302	TTTTATCAAAAAAAAAAAAAAAAAA	4332

RESULT 4

US-09-149-476-75
Sequence 75, Application US/09149476

Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476

Query Match 2.1%; Score 30; DB 4; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 30; Conservative 0; Mismatches 0; Indels

RESULT 5

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RES001.3
US-09-387-212-12
; Sequence 12, Application US/09387212A
; Patent No. 6309849
; GENERAL INFORMATION:
; APPLICANT: ROBISON, KEITH E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; FILE REFERENCE: MNI-090
; CURRENT APPLICATION NUMBER: US/09/387.212A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 12
; LENGTH: 1448
; TYPE: DNA

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OV 1367 TTATCAAAAAAAAAAAAAAAAAA 1396

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EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 2.1% Score 29; DB 4; Length 732;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1368 TATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
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DB 673 TATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 701

RESULT 10
US-09-615-192A-94
Sequence 94, Application US/09615192A
Patent No. 6410718
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003c40
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 94
LENGTH: 1012
TYPE: DNA
ORGANISM: Pinus radiata
US-09-615-192A-94

Query Match 2.1% Score 29; DB 4; Length 1012;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1368 TATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
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DB 984 TATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1012

RESULT 11
US-08-713-000-6
Sequence 6, Application US/08713000
Patent No. 5850020
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
APPLICANT: Grierson, Alastair
TITLE OF INVENTION: MATERIALS AND METHODS FOR THE
TITLE OF INVENTION: MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Speckman Picard PLLC
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,000
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1026 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-713-000-6

Query Match 2.1% Score 29; DB 2; Length 1026;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1368 TATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
|||||
DB 998 TATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1026

RESULT 12
US-08-975-316-6
Sequence 6, Application US/08975316
Patent No. 5952486
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N., Havukkala, Ilkka
APPLICANT: and Grierson, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185

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; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,316
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,000
; FILING DATE: September 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SLEATH, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000/1003C1
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1026 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-975-316-6

Query Match      2.1%  Score 29; DB 2; Length 1026;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 998 TATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1026

RESULT 13
US-09-211-710-6
; Sequence 6, Application US/09211710A
; Patent No. 6204434
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Grierson, Alastair
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1003c3
; CURRENT APPLICATION NUMBER: US/09/211,710A
; CURRENT FILING DATE: 1998-12-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Pinus radiata
; US-09-211-710-6

Query Match      2.1%  Score 29; DB 4; Length 1026;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 998 TATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1026

RESULT 14
US-09-615-192A-6
; Sequence 6, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1003c4U
; CURRENT APPLICATION NUMBER: US/09/615,192A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Pinus radiata
; US-09-615-192A-6

Query Match      2.1%  Score 29; DB 4; Length 1026;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1368 TATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
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Db 998 TATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1026

RESULT 15
US-08-605-106-3
; Sequence 3, Application US/08605106
; Patent No. 5910631
; GENERAL INFORMATION:
; APPLICANT: Topfer, R.
; APPLICANT: Martini, N.
; APPLICANT: Scheil, J.
; TITLE OF INVENTION: MEDIUM CHAIN-SPECIFIC THIOESTERS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,106
; FILING DATE: 23-SEPT-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/02935
; FILING DATE: 01-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 235.001US1
; TELEPHONE: 612-373-6900
; TELEFAX: 612-339-3061
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1066 Base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: : c-DNA to m-RNA
; HYPOTHETICAL: No
; ANTI-SENSE: No
; ORIGINAL SOURCE:
; ORGANISM: Cuphea lanceolata
; IMMEDIATE SOURCE:
; LIBRARY: c-DNA Bank ZAP
; CLONE: CITE12
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..875
; FEATURE:
; NAME/KEY: Stopcodon
; LOCATION: 876..878
US-08-605-106-3

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Query Match      2.1%; Score 29; DB 2; Length 1066;
Best Local Similarity 100.0%; Pred. NO. 0.0015;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1368 TATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
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Db 1028 TATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1056

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Search completed: February 2, 2003, 21:02:57
Job time : 93 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 21:01:29 : Search time 78 Seconds

(without alignments)
8040.688 Million cell updates/sec

Title: US-09-807-867-1
Perfect score: 1396
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Gapop 60.0 , Gapext 60.0

Searched: 396772 seqs, 224632407 residues

Word size : 0

Total number of hits satisfying chosen parameters: 793544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
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- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	39	2.8	215	10	Sequence 418, App
C 3	31	2.2	1280	10	Sequence 66, Appl
C 4	31	2.2	1617	12	US-09-770-445-21
C 5	31	2.2	2243	10	Sequence 21, Appl
C 6	31	2.2	2485	10	Sequence 4, Appli
C 7	30	2.1	995	10	Sequence 43, Appl
C 8	30	2.1	1492	9	Sequence 451, App
C 9	30	2.1	2478	9	Sequence 244, App
C 10	30	2.1	2478	9	Sequence 112, App
C 11	30	2.1	2478	9	Sequence 176, App
C 12	30	2.1	2478	9	Sequence 476, App
C 13	30	2.1	2478	9	Sequence 476, App
C 14	30	2.1	2478	9	Sequence 476, App
C 15	30	2.1	2478	9	Sequence 107, App
C 16	30	2.1	2478	9	Sequence 107, App
C 17	30	2.1	2478	12	US-10-052-586-107
C 18	30	2.1	2493	9	Sequence 107, App
C 19	30	2.1	2645	10	Sequence 63, Appl
					Sequence 76, Appl

20	29	2.1	297	10	US-09-867-701-9931
C 21	29	2.1	372	10	US-09-880-107-544
C 22	29	2.1	463	10	US-09-770-444-374
C 23	29	2.1	638	10	US-09-764-869-351
C 24	29	2.1	777	10	US-09-809-545A-42
C 25	29	2.1	814	9	US-10-202-193-257
C 26	29	2.1	1004	10	US-09-770-445-228
C 27	29	2.1	1129	10	US-09-925-301-235
C 28	29	2.1	1912	10	US-09-800-729-32
C 29	29	2.1	2208	10	US-09-925-297-365
C 30	29	2.1	2669	10	US-09-764-864-276
C 31	29	2.1	7002	10	US-09-954-456-1247
C 32	29	2.1	23934	10	US-09-764-860-777
C 33	29	2.1	23934	10	US-09-764-877-2536
C 34	29	2.1	23934	10	US-09-764-877-2544
C 35	29	2.1	32185	10	US-09-764-877-3171
C 36	28	2.0	45	10	US-09-827-289-13
C 37	28	2.0	45	10	US-09-827-289-17
C 38	28	2.0	57	9	US-10-007-357-4
C 39	28	2.0	92	12	US-10-029-913-3
C 40	28	2.0	171	9	US-10-046-935-584
C 41	28	2.0	171	9	US-09-878-178-584
C 42	28	2.0	173	9	US-10-015-219-1063
C 43	28	2.0	173	10	US-09-777-564-1063
C 44	28	2.0	173	10	US-09-867-701-9541
C 45	28	2.0	186	10	US-09-770-696-254

ALIGNMENTS

RESULT 1
US-09-770-445-418/c
; Sequence 418, Application US/09770445
; Patent No. US20020023281A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka,
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2023US (PARA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 418
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-445-418

Query Match 62.3%; Score 870; DB 10; Length 921;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 920; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 401 CTCTTCAACTAGTGGCTTTTGGACATGGATCATCAAGCTTGACGAAGAGTGAATGTTT 460
Db 921 CTCTTCAACTAGTGGCTTTTGGACATGGATCATCAAGCTTGACGAAGAGTGAATGTTT 862
QY 461 TCCTTACAGACTGGTATTAAAGTACTTGCACACTTTGTATGTCGACCGAACAATGCAA 520
Db 861 TCCTTACAGACTGGTATTAAAGTACTTGCACACTTTGTATGTCGACCGAACAATGCAA 802
QY 521 GGTTCCTTGTCTTGTAGACAAATTCGTAGAGTGCCTTATTTGGTGTATGTCGTGCTAC 580
Db 801 GGTTCCTTGTCTTGTAGACAAATTCGTAGAGTGCCTTATTTGGTGTATGTCGTGCTAC 742
QY 581 ATATGATGAGACTTGTGGTGTGGAGGAGCAGATTTATTTGAAGTACACTTTGTGTCG 640
Db 741 ATATGATGAGACTTGTGGTGTGGAGGAGCAGATTTATTTGAAGTACACTTTGTGTCG 682
QY 641 AGAGCTGGAATGAATGCATCACTTCTCATATGAAGAAATGGTGAATTTCTTGT 700
Db 681 AGAGCTGGAATGAATGCATCACTTCTCATATGAAGAAATGGTGAATTTCTTGT 622
QY 701 GGTTCATGCTTTTCTGGTCTAGCAGACATAGCAACCTTCTACTTCTATGACAGTGTCT 760
Db 621 GGTTCATGCTTTTCTGGTCTAGCAGACATAGCAACCTTCTACTTCTATGACAGTGTCT 562
QY 761 TGTATATCTTAAGCCCTAGAAATGAGATGATCTTTTCGGAATGTGCGAGAGTCAATGAT 820
Db 561 TGTATATCTTAAGCCCTAGAAATGAGATGATCTTTTCGGAATGTGCGAGAGTCAATGAT 502
QY 821 ATCAGACTTATGATTAATTTCTCAAGCCAGTGGAGAGGAGTTGAAGATATGCTGTCAC 880
Db 501 ATCAGACTTATGATTAATTTCTCAAGCCAGTGGAGAGGAGTTGAAGATATGCTGTCAC 442
QY 881 CGGATATCGCAGTAAATATCTATACGGGAGTGCCTTGTACTTATTTGATGAGTTCCAAA 940
Db 441 CGGATATCGCAGTAAATATCTATACGGGAGTGCCTTGTACTTATTTGATGAGTTCCAAA 382
QY 941 CATCAGAACTCCCAATATCTCAAGACCAAGTAAATAGAAAATCTATACGATGTGTTGTA 1000
Db 381 CATCAGAACTCCCAATATCTCAAGACCAAGTAAATAGAAAATCTATACGATGTGTTGTA 322
QY 1001 ACATAGAGATGATGAAGCAGAACACTGCAAGACATGAGAGCTTGTGACAGTCTAGGCA 1060
Db 321 ACATAGAGATGATGAAGCAGAACACTGCAAGACATGAGAGCTTGTGACAGTCTAGGCA 262
QY 1061 GTCGTGCTTCCACACTCCATTTTAGATGATGATGATGATGATGATGATGATGATGATG 1120
Db 261 GTCGTGCTTCCACACTCCATTTTAGATGATGATGATGATGATGATGATGATGATGATG 202
QY 1121 TTGTTCTCAGGAGGCTCATTCGGAAGGTATTTGTAGACTGCTCAAGAAATCCATTACAA 1180
Db 201 TTGTTCTCAGGAGGCTCATTCGGAAGGTATTTGTAGACTGCTCAAGAAATCCATTACAA 142
QY 1181 GTTAATAAATAGAAAGTAACTAAAGAAATTTATTTGATCAGCTCATGAACAATGAT 1240
Db 141 GTTAATAAATAGAAAGTAACTAAAGAAATTTATTTGATCAGCTCATGAACAATGAT 82
QY 1241 ATAATCCCATATCTTGGGAATTAAGGAATTAATGTGAATTTCCCATGCTTGTGCTAGTGT 1300
Db 81 ATAATCCCATATCTTGGGAATTAAGGAATTAATGTGAATTTCCCATGCTTGTGCTAGTGT 22
QY 1301 GTGAGAGATCAATACCCCTA 1321
Db 21 GTGAGAGATCAATACCCCTA 1

RESULT 2

US-09-770-696-66/c
; Sequence 66, Application US/09770696
; Patent No. US2001004490A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jorn
; APPLICANT: An, Yong-Qiang

; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Ted
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE OF INVENTION: thaliana
; FILE REFERENCE: 2031US (PARA-020PRV)
; CURRENT APPLICATION NUMBER: US/09/770,696
; CURRENT FILING DATE: 2001-01-26
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 911
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 215
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-696-66

Query Match 2.8%; Score 39; DB 10; Length 215;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 GACGGAGATGGCGCGATTTTCAGGCATCTCTCTGCTAC 161
|||||
Db 52 GACGGAGATGGCGCGATTTTCAGGCATCTCTCTGCTAC 14

RESULT 3

US-09-770-445-21/c

; Sequence 21, Application US/09770445

; Patent No. US2002023281A1

; GENERAL INFORMATION:

; APPLICANT: Goriach, Jorn

; APPLICANT: An, Yong-Qiang

; APPLICANT: Hamilton, Carol M.

; APPLICANT: Price, Jennifer L.

; APPLICANT: Raines, Tracy M.

; APPLICANT: Yu, Yang

; APPLICANT: Rameaka, Joshua G.

; APPLICANT: Page, Amy

; APPLICANT: Matthew, Abraham V.

; APPLICANT: Ledford, Brooke L.

; APPLICANT: Woessner, Jeffrey P.

; APPLICANT: Haas, William David

; APPLICANT: Garcia, Carlos A.

; APPLICANT: Kricker, Ted

; APPLICANT: Slader, Ted

; APPLICANT: Davis, Keith R.

; APPLICANT: Allen, Keith

; APPLICANT: Hoffman, Neil

; APPLICANT: Hurban, Patrick

; TITLE OF INVENTION: Expressed Sequences of Arabidopsis

; FILE OF INVENTION: thaliana

; FILE REFERENCE: 2023US (PARA-012PRV)

; CURRENT APPLICATION NUMBER: US/09/770,445

; CURRENT FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: US 60/178,472

; PRIOR FILING DATE: 2000-01-27

; NUMBER OF SEQ ID NOS: 999

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1280
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1280)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-445-21
```

```
Query Match 2.2%; Score 31; DB 10; Length 1280;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1365 TTTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1395
|||||
Db 31 TTTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1
```

RESULT 4

```
US-10-093-045-4
; Sequence 4, Application US/10093045
; Patent No. US20020151708A1
; GENERAL INFORMATION:
; APPLICANT: Guerriero, Vincent
; APPLICANT: Raynes, Deborah A
; TITLE OF INVENTION: DNA Encoding Proteins That Inhibit Hsp70 Function
; FILE REFERENCE: HspBP DNA and Protein Sequences
; CURRENT APPLICATION NUMBER: US/10/093,045
; CURRENT FILING DATE: 2002-03-07
; EARLIER APPLICATION NUMBER: 09/444,336
; EARLIER FILING DATE: 1999-11-19
; EARLIER APPLICATION NUMBER: 60/109,351
; EARLIER FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1617
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-093-045-4
```

```
Query Match 2.2%; Score 31; DB 12; Length 1617;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1366 TTTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
|||||
Db 1587 TTTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1617
```

RESULT 5

```
US-09-764-864-43
; Sequence 43, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 2243
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-43
```

```
Query Match 2.2%; Score 31; DB 10; Length 2243;
Best Local Similarity 100.0%; Pred. No. 0.0018;
```

```
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1366 TTTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
|||||
Db 2209 TTTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 2239
```

RESULT 6

```
US-09-925-300-451
; Sequence 451, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 451
; LENGTH: 2485
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (222)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-451
```

```
Query Match 2.2%; Score 31; DB 10; Length 2485;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1366 TTTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
|||||
Db 2438 TTTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 2468
```

RESULT 7

```
US-09-770-445-244/C
; Sequence 244, Application US/09770445
; Patent No. US20020023281A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurlban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2023US (PARA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
```

; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 244
; LENGTH: 995
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-445-244

Query Match 2.1%; Score 30; DB 10; Length 995;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1367 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
|||||
DB 52 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 23

RESULT 8

US-09-925-299-112
; Sequence 112, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PAL02
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 112
; LENGTH: 1492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1487)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1491)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-112

Query Match 2.1%; Score 30; DB 10; Length 1492;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1367 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
|||||
DB 1363 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1392

RESULT 9

US-09-978-295A-476
; Sequence 476, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31

; PRIOR APPLICATION NUMBER: 60/080107
 ; PRIOR FILING DATE: 1998-03-31
 ; PRIOR APPLICATION NUMBER: 60/080165
 ; PRIOR FILING DATE: 1998-03-31
 ; PRIOR APPLICATION NUMBER: 60/080194
 ; PRIOR FILING DATE: 1998-03-31
 ; PRIOR APPLICATION NUMBER: 60/080327
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/080328
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/080333
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/080334
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/081070
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081049
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081071
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081195
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081203
 ; PRIOR FILING DATE: 1998-04-09
 ; PRIOR APPLICATION NUMBER: 60/081229
 ; PRIOR FILING DATE: 1998-04-09
 ; PRIOR APPLICATION NUMBER: 60/081955
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081817
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081819
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081952
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081838
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/082568
 ; PRIOR FILING DATE: 1998-04-21
 ; PRIOR APPLICATION NUMBER: 60/082569
 ; PRIOR FILING DATE: 1998-04-21
 ; PRIOR APPLICATION NUMBER: 60/082704
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082804
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082700
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082797
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082796
 ; PRIOR FILING DATE: 1998-04-23
 ; PRIOR APPLICATION NUMBER: 60/083336
 ; PRIOR FILING DATE: 1998-04-27
 ; PRIOR APPLICATION NUMBER: 60/083322
 ; PRIOR FILING DATE: 1998-04-28
 ; PRIOR APPLICATION NUMBER: 60/083392
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083495
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083496
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083499
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083545
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083554
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083558
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083559
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083500
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083742

; PRIOR FILING DATE: 1998-04-30
 ; PRIOR APPLICATION NUMBER: 60/084366
 ; PRIOR FILING DATE: 1998-05-05
 ; PRIOR APPLICATION NUMBER: 60/084414
 ; PRIOR FILING DATE: 1998-05-06
 ; PRIOR APPLICATION NUMBER: 60/084441
 ; PRIOR FILING DATE: 1998-05-06
 ; PRIOR APPLICATION NUMBER: 60/084637
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084639
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084640
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084598
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084600
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084627
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084643
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/085339
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085338
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085323
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085582
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085700
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085689
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085579
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085580
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 2.1%; Score 30; DB 9; Length 2478;

Best Local Similarity 100.0%; Pred. No. 0.0045;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1367 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1396

Db 2437 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2466

RESULT 10

US-09-978-697-476
 ; Sequence 476, Application US/09978697
 ; Patent No. us20020169284A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.

APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane polypeptides and Nucleic
FILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/085697

Query Match 2.1% Score 30; DB 9; Length 2478;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1367 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
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DB 2437 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2466
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RESULT 11
US-09-978-192A-476
Sequence 476, Application US/09978192A
Patent No. US2002017553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 2.1%; Score 30; DB 9; Length 2478;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1367 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
Db 2437 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2466

RESULT 12

US-09-999-832A-476
; Sequence 476, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC63

[illegible]

;> PRIOR APPLICATION NUMBER: 60/085339
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Query Match 2.1%; Score 30; DB 9; Length 2478;

Best Local Similarity 100.0%; Pred.No. 0.0045;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1367 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1396

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Db 2437 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2466

RESULT 13

US-09-978-189-476

; Sequence 476, Application US/09978189

; Publication No. US20030004102A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
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; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paonli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC7
; CURRENT APPLICATION NUMBER: US/09/978,189
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; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
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; PRIOR APPLICATION NUMBER: 60/084600
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; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 2.1%; Score 30; DB 9; Length 2478;

Best Local Similarity 100.0%; Pred. No. 0.0045; Mismatches 0; Gaps 0;

QY 1367 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
|||||
Db 2437 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 2466

RESULT 14

US-10-174-590-107
; Sequence 107, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 107
; LENGTH: 2478
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-107

Query Match 2.1%; Score 30; DB 9; Length 2478;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Mismatches 0; Gaps 0;

QY 1367 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 1396
|||||
Db 2437 TTATCAAAAAAAAAAAAAAAAAAAAAAAAAA 2466

RESULT 15

US-10-176-758-107
; Sequence 107, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.

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; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 107
; LENGTH: 2478
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-758-107

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Query Match      2.1%; Score 30; DB 9; Length 2478;
Best Local Similarity 100.0%; Pred. NO. 0.0045;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1367 TTATCAAAAAAAAAAAAAAAAAAAAAAA 1396
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Db 2437 TTATCAAAAAAAAAAAAAAAAAAAAAAA 2466

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Search completed: February 2, 2003, 22:44:41
Job time : 115 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 20:58:55 ; Search time 2242 Seconds
(without alignments)
10084.255 Million cell updates/sec

Title: US-09-807-867-1
Perfect score: 1396
Sequence: 1 ccgcacattgggttcgt.....aaaaaaaaaaaaaaaaaaaaa 1396

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
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9: gb_estl.*
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11: gb_htc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
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20: em_gss_pln.*
21: em_gss_vrt.*
22: em_gss_fun.*
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24: em_gss_mus.*
25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_rod.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	556	39.8	574	10	AV829185
2	466	33.4	721	10	BE038851
3	449	32.2	630	10	AV440012
4	398	28.5	398	10	AV536756
5	394	28.2	579	9	A1997645
6	282	20.2	432	10	AV798458

c	7	277	19.8	413	10	AV814996
c	8	268	19.2	472	9	A1994896
c	9	253	18.1	253	10	AV562439
c	10	235	16.8	422	10	AV808193
c	11	232	16.6	261	10	BE527658
c	12	218	15.6	284	10	BE522866
c	13	173	12.4	173	10	AV441747
c	14	131	9.4	376	10	AV804850
c	15	130	9.3	1166	17	B09762
c	16	93	6.7	520	10	AV544091
c	17	91	6.5	426	14	T42793
c	18	88	6.3	171	10	AV552557
c	19	84	6.0	415	9	AA395166
c	20	63	4.5	267	14	R30022
c	21	48	3.4	670	17	BH563128
c	22	37	2.7	300	12	BG511663
c	23	35	2.5	276	10	BE057322
c	24	35	2.5	353	9	AI074729
c	25	34	2.4	222	13	BM565902
c	26	34	2.4	238	13	BM566385
c	27	33	2.4	275	12	BF777697
c	28	33	2.4	357	10	AW415996
c	29	33	2.4	394	10	BE668854
c	30	33	2.4	399	10	AV806414
c	31	33	2.4	470	13	BI945764
c	32	33	2.4	483	13	BM396187
c	33	33	2.4	510	10	BE030519
c	34	33	2.4	601	14	BQ522145
c	35	33	2.4	670	14	BQ412053
c	36	33	2.4	752	12	BG440527
c	37	33	2.4	864	12	BG167921
c	38	33	2.4	1739	11	AV104099
c	39	32	2.3	68	9	AJ281323
c	40	32	2.3	82	9	A1540303
c	41	32	2.3	124	14	BQ792800
c	42	32	2.3	168	13	BI945315
c	43	32	2.3	172	13	BI316657
c	44	32	2.3	173	14	BQ799719
c	45	32	2.3	191	12	BG893813

ALIGNMENTS

RESULT 1
AV829185
LOCUS
DEFINITION
AV829185 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-40-M04 5', mRNA linear EST 01-APR-2002
mRNA sequence.
ACCESSION
AV829185
VERSION
AV829185.1
KEYWORDS
GI:19871245
SOURCE
EST.
ORGANISM
Arabidopsis thaliana
thale cress.
REFERENCE
1 (bases 1 to 574)
AUTHORS
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.
TITLE
Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL
Unpublished (2002)
COMMENT
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI

AV814996	AV814996
A1994896	701500351
AV562439	AV562439
AV808193	AV808193
BE527658	M29G11STM
BE522866	M29G11STM
AV441747	AV441747
AV804850	AV804850
B09762	P24K2-Sp6 I
AV544091	AV544091
T42793	6056 Lambda
AV552557	AV552557
AA395166	26963 Lam
R30022	12627 Lambd
BM563128	BOGLG18TF
BG511663	sa09B07
BE057322	sn01e09.Y
AI074729	ox83g04.s
BM565902	rt04f04.Y
BM566385	rt04f04.Y
BF777697	NXSI-073
AW415996	50850 MAR
BE668854	159239 MA
AV806414	AV806414
BI945764	sc68g02.Y
BM396187	5009-0-18
BE030519	128620 MA
BQ522145	N1SC-nl15
BQ412053	GA_Ea000
BG440527	GA_Ea000
BG167921	602340006
AV104099	zea mays
AJ281323	4A3A-P2A1
A1540303	tc34006.x
BQ792800	EST 7705
BI945315	sb55d03.Y
BI316657	sa71c01
BQ799719	EST 1888
BG893813	kt15g01.Y

and XhoI was ligated to modified Lambda FLC-1 vector (Carinci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES	Location/Qualifiers
source	1. .574
	/organism="Arabidopsis thaliana"
	/db_xref="taxon:3702"
	/clone="RAFL09-40-M04"
	/clone_lib="RAFL9"
	/dev_stage="plants at various developmental stages from germination to mature seeds"
	/lab_host="DHI08"
	/note="Site_1: BamHI; Site_2: SalI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"
BASE COUNT	142 a 131 c 119 g 182 t
ORIGIN	

	Query Match	39.8%; Score 556; DB 10; Length 574;	
	Best Local Similarity 100.0%; Pred. No. 5,6e-126;		
	Matches 556; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	CCGCTCACATGGGATTTCGTCAATCTTCTTAAACCCCGCAAATTTCTCCATTTCCTAC	60
Db			
	19	CCGCTCACATGGGATTTCGTCAATCTTCTTAAACCCCGCAAATTTCTCCATTTCCTAC	78
QY	61	C AAAAATAATCCAACCTTTACTTTCTTGTAAGAAATATCTGCCTCAAAATCTTTGGTTC	120
Db	79	C AAAAATAATCCAACCTTTACTTTCTTGTAAGAAATATCTGCCTCAAAATCTTTGGTTC	138
QY	121	CTCAGCGAGATGGCGGCGATTTCAGGCATCTCCTCTCGTGGTAGCATTTACGGCCT	180
Db	139	CTCAGCGAGATGGCGGCGATTTCAGGCATCTCCTCTCGTGGTAGCATTTACGGCCT	198
QY	181	TTGGTTACTCTTCAGCGCTCTAGACCGCGGTTTCGTACAGCTCCTCTCACCGATTGCTT	240
Db	199	TTGGTTACTCTTCAGCGCTCTAGACCGCGGTTTCGTACAGCTCCTCTCACCGATTGCTT	258
QY	241	CATCATCTTCCTCTCTCTCTCGTCGTGCTATTAAGGAACAATCATCGAGTCCCAAGCA	300
Db	259	CATCATCTTCCTCTCTCTCTCGTCGTGCTATTAAGGAACAATCATCGAGTCCCAAGCA	318
QY	301	ACGATTTTGC AAGCATGAAGAAGTGGTGGTGAGGAATCGTTTAAAGCCGAGACT	360
Db	319	ACGATTTTGC AAGCATGAAGAAGTGGTGGTGAGGAATCGTTTAAAGCCGAGACT	378
QY	361	TCTACTGGTACAGAACCCTTTGAGGAGCCAAATATAGATTCTTCTTCAACTAGTGCCTTT	420
Db	379	TCTACTGGTACAGAACCCTTTGAGGAGCCAAATATAGATTCTTCTTCAACTAGTGCCTTT	438
QY	421	GAGACATGGATCATCAAGCTTGAGCAAGGAGTGAATGTTTTCTCTTACAGACTCGGTATT	480
Db	439	GAGACATGGATCATCAAGCTTGAGCAAGGAGTGAATGTTTTCTCTTACAGACTCGGTATT	498
QY	481	AAGATACTTGCACACTTTGTATCGTGACGCAACATATGCAAGGTTCTTTGTCTTTGAGACA	540
Db	499	AGATACTTGCACACTTTGTATCGTGACGCAACATATGCAAGGTTCTTTGTCTTTGAGACA	558
QY	541	ATTGCTAGAGTGCCTT	556
Db	559	ATTGCTAGAGTGCCTT	574

RESULT 2	BEQ38851	721 bp	linear	EST 07-JUN-2000
LOCUS	AB05A07	Arabidopsis thaliana	cDNA 5'	similar to mutants, mRNA
DEFINITION	BEQ38851	sequence.		
ACCESSION	BEQ38851			
VERSION	BEQ38851.1			
KEYWORDS	EST.			

SOURCE ORGANISM

REFERENCE AUTHORS

TITLE	JOURNAL	COMMENT
1. The Role of the Teacher in the Classroom	Journal of Educational Research	1965, Vol. 68, No. 1, pp. 1-10
2. The Impact of Technology on Education	Journal of Educational Research	1965, Vol. 68, No. 2, pp. 11-20
3. The Importance of Parental Involvement	Journal of Educational Research	1965, Vol. 68, No. 3, pp. 21-30
4. The Effect of Student Motivation on Learning	Journal of Educational Research	1965, Vol. 68, No. 4, pp. 31-40
5. The Role of the School in Society	Journal of Educational Research	1965, Vol. 68, No. 5, pp. 41-50
6. The Impact of Teacher Education on Classroom Practice	Journal of Educational Research	1965, Vol. 68, No. 6, pp. 51-60
7. The Importance of Professional Development	Journal of Educational Research	1965, Vol. 68, No. 7, pp. 61-70
8. The Effect of Curriculum Reform on Student Achievement	Journal of Educational Research	1965, Vol. 68, No. 8, pp. 71-80
9. The Role of the School in Promoting Social Change	Journal of Educational Research	1965, Vol. 68, No. 9, pp. 81-90
10. The Impact of Teacher Attitudes on Student Behavior	Journal of Educational Research	1965, Vol. 68, No. 10, pp. 91-100

FEATURES	SOURCE
1. <i>General</i>	
2. <i>Specific</i>	
3. <i>Other</i>	
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BASE COUNT
ORIGIN

Query Match 33.4%; Score 466; DB 10; Length 721;
Best Local Similarity 99.8%; Pred. No. 2.9e-104;
Matches 516; Conservative 0; Mismatches 1; Indels 0

QY 698 GGTGGTTTGATCGTTTCTTGGCTCAGCACATAGCAACCTTCTACTTCTCATGCACAGTGT 757

Db 7 GTGGTTTGATCGTTTCTCTGGCTCAGCACATAGCAACCTTCTACTACTTCATGCAGTGT 66

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DB 67 TCTTGATATATCTTTAAGCCCTAGAAATGGCATATCACCTTTTCGGAATGCTGGAGAGTCATG 126

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AV440012/c
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630 bp mRNA linear EST 14-NOV-2000

LOCUS AV440012

EST.

KEYWORDS

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Db	180	TACATATGATGAGACCTTTGGTTGGTGAGAGAGAGACAGATTATTTGAAAGTACACATTTG	239
Qy	638	CTGAGAGCTGAATGAATGATGATCCTTCTGCTCAATAAGGAAGATTGGTGGGAATTCCT	697
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VERSION			
AV562439.1 GI:8733865			
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SOURCE			
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ORGANISM			
Arabidopsis thaliana			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.			
REFERENCE			
AUTHORS			
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.			
TITLE			
A large scale analysis of cDNA in Arabidopsis thaliana: Generation			
of 12,028 non-redundant expressed sequence tags from normalized and			
size-selected cDNA libraries			
JOURNAL			
DNA Res. 7, 175-180 (2000)			
MEDLINE			
20363093			
COMMENT			
Contact: Erika Asamizu			
The First Laboratory for Plant Gene Research			
Kazusa DNA Research Institute			
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan			
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.			
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Db 184 GAGGAGGCTCAATCGGAGGATTTGTAGACTGCTCAAGAAATCCATTACAAGTTAATA 125
QY 1189 ATTAGAAGTAACTAAAAAGATTTATTGTATCAGCTCATGAACAATAGATATAATCCC 1248
Db 124 ATTAGAAGTAACTAAAAAGATTTATTGTATCAGCTCATGAACAATAGATATAATCCC 65
QY 1249 ATATACTTGGGAATAAAGGAATAATGTGAATTTCCCA 1285
Db 64 ATATACTTGGGAATAAAGGAATAATGTGAATTTCCCA 28

RESULT 11
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LOCUS M69K21STM Arabidopsis developing seed Arabidopsis thaliana cDNA
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VERSION BE527658
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
JOURNAL White,J.A., Todd,J., Newman,T., Focks,N., Girke,T., Martinez de
MEDLINE Ilarduya,O., Jaworski,J.G., Ohlrogge,J. and Benning,C.
COMMENT A new set of Arabidopsis expressed sequence tags from developing
seeds. The metabolic pathway from carbohydrates to seed oil
Plant Physiol. 124 (4), 1582-1594 (2000)
20567808
Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI 48824
, USA
Tel: 517 355 1609
Fax: 517 353 9334
Email: benning@msu.edu
Clones were originally prepared at Michigan State University.
Arabidopsis Biological Resource Center, The Ohio State University,
309 Botany & Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210
USA, FAX: 6142920603 TEL: 6142929371.
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.8e-47;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTCACATGGGATTCGTCATTCTTCTTAAACCCGCAAAATTTCTCCATTCTAC 60
Db 30 CCGCTCACATGGGATTCGTCATTCTTCTTAAACCCGCAAAATTTCTCCATTCTAC 89
QY 61 CAAATAATCAACTTTTACTTTTCTTCTGTGAAATTTATCTGCTCAAAATCTTTGGTTC 120
Db 61 CAAATAATCAACTTTTACTTTTCTTCTGTGAAATTTATCTGCTCAAAATCTTTGGTTC 135
QY 121 CTGACGGAGATGGCGCGATTTTACGATCTCTCTGTGAAATTTACGATTTTCACGGCT 180
Db 136 CTGACGGAGATGGCGCGATTTTACGATCTCTCTGTGAAATTTACGATTTTCACGGCT 195
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Db 90 CAAAAATATCAACTTTTACTTTTCTTCTGTGAAATTTATCTGCTCAAAATCTTTGGTTC 149
QY 121 CTGACGGAGATGGCGCGATTTTACGATCTCTCTGTGAAATTTATCTGCTCAAAATCTTTGGTTC 180
Db 150 CTGACGGAGATGGCGCGATTTTACGATCTCTCTGTGAAATTTATCTGCTCAAAATCTTTGGTTC 209
QY 181 TTGGTTACTTCTTCGAGCGCTCTAGAGCGCGGTTTTCGTACAGCTCTCTCTCACC 232
Db 210 TTGGTTACTTCTTCGAGCGCTCTAGAGCGCGGTTTTCGTACAGCTCTCTCTCACC 261

RESULT 12
BE522866 284 bp mRNA linear EST 19-MAR-2001
LOCUS M29G11STM Arabidopsis developing seed Arabidopsis thaliana cDNA
DEFINITION
ACCESSION BE522866
VERSION BE522866
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
JOURNAL White,J.A., Todd,J., Newman,T., Focks,N., Girke,T., Martinez de
MEDLINE Ilarduya,O., Jaworski,J.G., Ohlrogge,J. and Benning,C.
COMMENT A new set of Arabidopsis expressed sequence tags from developing
seeds. The metabolic pathway from carbohydrates to seed oil
Plant Physiol. 124 (4), 1582-1594 (2000)
20567808
Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI 48824
, USA
Tel: 517 355 1609
Fax: 517 353 9334
Email: benning@msu.edu
Clones were originally prepared at Michigan State University.
Arabidopsis Biological Resource Center, The Ohio State University,
309 Botany & Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210
USA, FAX: 6142920603 TEL: 6142929371.
Location/Qualifiers
FEATURES
source
1. .284
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="M29G11"
/tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.coli"
/note="Organ: Developing seed; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 55 a 83 c 49 g 96 t
ORIGIN
Query Match 15.6%; Score 218; DB 10; Length 284;
Best Local Similarity 99.6%; Pred. No. 8.7e-44;
Matches 268; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGCTCACATGGGATTCGTCATTCTTCTTAAACCCGCAAAATTTCTCCATTCTAC 60
Db 16 CCGCTCACATGGGATTCGTCATTCTTCTTAAACCCGCAAAATTTCTCCATTCTAC 75
QY 61 CAAAAATATCAACTTTTACTTTTCTTCTGTGAAATTTATCTGCTCAAAATCTTTGGTTC 120
Db 76 CAAAAATATCAACTTTTACTTTTCTTCTGTGAAATTTATCTGCTCAAAATCTTTGGTTC 135
QY 121 CTGACGGAGATGGCGCGATTTTACGATCTCTCTGTGAAATTTACGATTTTCACGGCT 180
Db 136 CTGACGGAGATGGCGCGATTTTACGATCTCTCTGTGAAATTTACGATTTTCACGGCT 195
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QY 181 TTGGTTACTCTTCGAGCGCTAGAGCCGCTTTCGTACAGTCTCTCTACCGATTGCTT 240
|||||
Db 196 TTGGTTACTCTTCGAGCGCTAGAGCCGCTTTCGTACAGTCTCTCTACCGATTGCTT 255
|||||

QY 241 CATCATCTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 269
|||||
Db 256 CATCATCTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 284
|||||

RESULT 13
AV441747
LOCUS
DEFINITION
  AV441747 Arabidopsis thaliana above-ground organ two to six-week
  old Arabidopsis thaliana cDNA clone APD34b10_r 5', mRNA sequence.
ACCESSION
  AV441747
VERSION
  AV441747.1 GI:7612140
KEYWORDS
  EST.
SOURCE
  Arabidopsis thaliana
  thale cress.
ORGANISM
  Arabidopsis thaliana
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Rosidae; euroids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 173)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
JOURNAL
  DNA Res. 7, 175-180 (2000)
MEDLINE
  20363093
COMMENT
  Contact: Erika Asamizu
  The First Laboratory for Plant Gene Research
  Kazusa DNA Research Institute
  Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
  Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
  source
  1..173
    /organism="Arabidopsis thaliana"
    /strain="Columbia"
    /db_xref="taxon:3702"
    /clone="APD34b10_r"
    /clone_lib="Arabidopsis thaliana above-ground organ two to
    six-week old"
    /tissue_type="aboveground organs"
    /dev_stage="two to six-week old"
    /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
    xhoI"
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    40 a 44 c 27 g 62 t
    ORIGIN
    Query Match
    Best Local Similarity 100.0%; Score 173; DB 10; Length 173;
    Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 4 CTCACATGGGATTCGTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 63
    |||||
  Db 1 CTCACATGGGATTCGTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
    |||||
  QY 64 AAATATCCAACCTTTTACCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 123
    |||||
  Db 61 AAATATCCAACCTTTTACCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
    |||||
  QY 124 ACGGAGATGGCGGCGATTTCAGGCATCTCCCTCTGTCAGTTGACGATTTTCACG 176
    |||||
  Db 121 ACGGAGATGGCGGCGATTTCAGGCATCTCCCTCTGTCAGTTGACGATTTTCACG 173
    |||||

RESULT 14
AV804850/c
LOCUS
DEFINITION
  AV804850 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-40-M04 3',
  mRNA sequence.
ACCESSION
  AV804850

```

```

AV804850.1 GI:19838835
EST.
SOURCE
  Arabidopsis thaliana
  thale cress.
ORGANISM
  Arabidopsis thaliana
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Rosidae; euroids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 376)
Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
and Shinozaki,K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rct.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
details.
FEATURES
  source
  1..376
    /organism="Arabidopsis thaliana"
    /db_xref="taxon:3702"
    /clone="RAFL09-40-M04"
    /clone_lib="RAFL9"
    /dev_stage="plants at various developmental stages from
    germination to mature seeds"
    /lab_host="DH10B"
    /note="Site_1: BamHI; Site_2: SalI; subjected to
    dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24
    hr) treatments"
  BASE COUNT
    104 a 77 c 59 g 136 t
    ORIGIN
    Query Match
    Best Local Similarity 99.5%; Score 131; DB 10; Length 376;
    Matches 181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
  QY 966 ACCAGTAATAGAAAATCTATACAGTGTGTTTGGAACATAAGAGATGATGAGCAACA 1025
    |||||
  Db 376 ACCAGTAATAGAAAATCTATACAGTGTGTTTGGAACATAAGAGATGATGAGCAACA 317
    |||||
  QY 1026 CTGCAAGACAATGAGAGCTGTGCAGACTCTAGCAGCTCTCCGTCCTCCACACTCCATTTT 1085
    |||||
  Db 316 CTGCAAGACAATGAGAGCTGTGCAGACTCTAGCAGCTCTCCGTCCTCCACACTCCATTTT 257
    |||||
  QY 1086 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1145
    |||||
  Db 256 AGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 197
    |||||
  QY 1146 AG 1147
    ||
  Db 196 AG 195

RESULT 15
B09762
LOCUS
DEFINITION
  B09762 F24K2-Sp6 IGF Arabidopsis thaliana genomic clone F24K2, DNA
  sequence.
ACCESSION
  B09762
VERSION
  B09762.1 GI:2090881
KEYWORDS
  GSS.
SOURCE
  thale cress.

```

ORGANISM

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
AUTHORS

1 (bases 1 to 1166)
Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and
Ecker, J.

TITLE

BAC End Sequences at ATGC

JOURNAL

Unpublished (1997)

COMMENT

Other_GSSs: F24K2-T7

Contact: Ecker, J.

Arabidopsis Thaliana Genome Center

University of Pennsylvania

Dept. of Biology, University of Pennsylvania, Philadelphia, PA

19104

Tel: 215-898-9384

Fax: 215-898-8780

Email: jecker@atgenome.bio.upenn.edu

Seq primer: Sp6

Class: BAC ends

High quality sequence start: 50

High quality sequence stop: 865.

FEATURES

source

Location/Qualifiers

1..1166

/organism="Arabidopsis thaliana"

/strain="Columbia"

/db_xref="taxon:3702"

/clone="F24K2"

/clone_lib="IGF"

/sex="hermaphrodite"

/note="Vector: BelOBACII; Site_1: EcoRI; Site_2: EcoRI;

Produced by Thomas Altmann"

315 a 232 c 218 g 399 t 2 others

BASE COUNT

315 a 232 c 218 g 399 t 2 others

ORIGIN

Query Match

Best Local Similarity 9.3%; Score 130; DB 17; Length 1166;

Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTCACATTCGGATTCGTCATTTCTTTCTTAAACCCGCAAAATTTCTCCATTTCTAC 60

Db 475 CCGCTCACATTCGGATTCGTCATTTCTTTCTTAAACCCGCAAAATTTCTCCATTTCTAC 534

QY 61 CAAAATATCCAACTTTTACITTTCTTTCCCTGTGAATTTATCTGCTCAAAATCTTTGGTTC 120

Db 535 CAAAATATCCAACTTTTACITTTCTTTCCCTGTGAATTTATCTGCTCAAAATCTTTGGTTC 594

QY 121 CTGACGGAGA 130

Db 595 CTGACGGAGA 604

Search completed: February 2, 2003, 22:42:54

Job time : 2265 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2003, 21:03:06 ; Search time 70 seconds
(without alignments)
668.157 Million cell updates/sec

Title: US-09-807-867-2
Perfect score: 1845
Sequence: 1 MAALISGSSGTLTISRPLVT.....VPEAHCEGIVDCIKRSITS 351

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1845	100.0	351	21	Terminal oxidase a
2	1739	94.3	335	23	Herbicidally activ
3	196.5	10.7	318	21	Arabidopsis thalia
4	194.5	10.5	282	23	Herbicidally activ
5	192	10.4	587	21	Arabidopsis thalia
6	192	10.4	593	21	Arabidopsis thalia
7	192	10.4	595	21	Arabidopsis thalia
8	191.5	10.4	347	21	An alternative oxi
9	187.5	10.2	242	21	Arabidopsis thalia
10	187.5	10.2	282	21	Arabidopsis thalia

11	187.5	10.2	329	21	AAG48768	Arabidopsis thalia
12	187.5	10.2	329	23	ABB92457	Herbicidally activ
13	187	10.1	287	23	ABB91225	Herbicidally activ
14	185.5	10.1	353	21	AAG49606	Arabidopsis thalia
15	185.5	10.1	354	21	AAG49605	Arabidopsis thalia
16	185.5	10.1	354	23	ABB92395	Herbicidally activ
17	185.5	10.1	386	21	AAG49604	Arabidopsis thalia
18	184	10.0	329	21	AAB08002	An alternative oxi
19	178.5	9.7	175	21	AAG22099	Arabidopsis thalia
20	178.5	9.7	179	21	AAG22098	Arabidopsis thalia
21	177	9.6	401	23	ABB76399	Phaffia rhodozyma
22	176.5	9.6	323	21	AAG49603	Arabidopsis thalia
23	176.5	9.6	324	21	AAG49602	Arabidopsis thalia
24	176.5	9.6	325	21	AAG49601	Arabidopsis thalia
25	176.5	9.6	325	23	ABB92394	Herbicidally activ
26	169.5	9.2	174	21	AAG44170	Arabidopsis thalia
27	169.5	9.2	175	21	AAG44169	Arabidopsis thalia
28	153.5	8.3	357	23	AAM50305	Pichia stipitis SH
29	151	8.2	164	21	AAG44171	Arabidopsis thalia
30	101.5	5.5	461	23	ABP27470	Streptococcus poly
31	100	5.4	444	21	AAB41810	Human OREF ORF1574
32	100	5.4	444	21	AA97539	Human fatty acid d
33	100	5.4	444	21	AA59182	Human oxidoreducta
34	100	5.4	444	22	AAE11083	Human delta-6-desa
35	100	5.4	444	22	AA93425	Human polypeptide,
36	100	5.4	473	22	AAE11084	C-terminal tagged
37	96	5.2	917	22	AU34107	Staphylococcus aur
38	96	5.2	920	22	AU36588	Staphylococcus aur
39	96	5.2	920	22	AU37402	Staphylococcus aur
40	96	5.2	920	22	AU37555	Staphylococcus aur
41	95	5.1	1252	22	ABB66357	Drosophila melanog
42	93.5	5.1	699	22	AB59209	Drosophila melanog
43	91.5	5.0	600	22	AB58933	Drosophila melanog
44	90.5	4.9	312	21	AAG08413	Arabidopsis thalia
45	90	4.9	1418	22	ABG02184	Novel human diagno

ALIGNMENTS

RESULT 1
AAY84869
ID AAY84869 standard; Protein: 351 AA.

AC AAY84869;

DT 08-AUG-2000 (first entry)

XX Terminal oxidase associated with biosynthesis of carotenoids.

XX Terminal oxidase; carotenoid biosynthesis; OTBC; phytoene desaturase;

XX carotenoid production; fruit colour; tomato; variegated leave;

XX Vitamin A precursor; beta-carotene; high light intensity; plant injury.

XX Arabidopsis thaliana.

XX Key Location/Qualifiers

FT Peptide 1..57

FT Cleavage-site 56..57 /note= "chloroplast transit signal peptide"

XX FR2784688-A1.

XX 21-APR-2000.

XX 20-OCT-1998; 98FR-0013283.

XX 20-OCT-1998; 98FR-0013283.

XX (UYGR-) UNIV GRENoble FOURIER JOSEPH.

XX Carol S, Kuntz M, Mache R, Coupland G, Stevenson D;

DR WPI; 2000-331435/29.
XX N-PSDB; AAA14951.
PT New DNA encoding terminal oxidase associated with biosynthesis of
PT carotenoids, useful for altering carotenoid content of plants, e.g.
PT changing fruit color -
XX
PS Claim 5; Fig 1; 34pp; French.
XX
CC The present sequence represents a protein that is a terminal oxidase
CC associated with biosynthesis of carotenoids (ORBC). The polypeptide
CC is associated with carotenoid biosynthesis. The enzyme is found in
CC chloroplast membranes, and is necessary for the function of phytoene
CC desaturase. The ORBC polynucleotide is used to increase carotenoid
CC production in plants, while its complement is used for antisense
CC inhibition of carotenoid biosynthesis, e.g. for modifying the color
CC of fruits such as tomatoes; to generate plants with variegated leaves
CC and to increase the content of the Vitamin A precursor beta-carotene
CC (which is also an anti-oxidant and colorant). Beta-Carotenoids also
CC protect plants against injury caused by high light intensity.
XX
SQ Sequence 351 AA;
Query Match 100.0%; Score 1845; DB 21; Length 351;
Best Local Similarity 100.0%; Pred. No. 9.9e-203;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAATGSSGTLTISRPLVTLRRSRAAVSYSSSHRLLHLLPLSSRLLLNHRVQATIL 60
DB 1 MAATGSSGTLTISRPLVTLRRSRAAVSYSSSHRLLHLLPLSSRLLLNHRVQATIL 60
QY 61 QDDEKVVVEESFKAETSTGTPELEPNMSSSTSAFETWIIKLEQGVNVLTDVSVIKIL 120
DB 61 QDDEKVVVEESFKAETSTGTPELEPNMSSSTSAFETWIIKLEQGVNVLTDVSVIKIL 120
QY 121 DTLYRDRTYARFFVLETIARVPYFAFMSVLHMYETFGWRRADYLVKVFHFAESWNEHHLL 180
DB 121 DTLYRDRTYARFFVLETIARVPYFAFMSVLHMYETFGWRRADYLVKVFHFAESWNEHHLL 180
QY 181 IMEELGNSWDFRFLAQHIAFYFMTVFLYILSPRMAYHFSECVESHAYETYDKFLKA 240
DB 181 IMEELGNSWDFRFLAQHIAFYFMTVFLYILSPRMAYHFSECVESHAYETYDKFLKA 240
QY 241 SGEELKNMPADIAVKYTTGGDLYLDFEQTSTRTPTNTRRPVNIENLYDVFNIRDDAEHC 300
DB 241 SGEELKNMPADIAVKYTTGGDLYLDFEQTSTRTPTNTRRPVNIENLYDVFNIRDDAEHC 300
QY 301 KTRACOTLGSLRSPHSIILDDDDTEESGCVVPEEAHCEGIVDCLKKSITS 351
DB 301 KTRACOTLGSLRSPHSIILDDDDTEESGCVVPEEAHCEGIVDCLKKSITS 351
RESULT 2
AB93048
ID AB93048 standard; Protein; 335 AA.
XX
AC AB93048;
XX
DT 31-MAY-2002 (first entry)
XX
DE Herbicidally active polypeptide SEQ ID NO 2259.
XX
KW Herbicidal; plant; agriculture; herbicide.
XX
OS Arabidopsis thaliana.
XX
PN WO200210210-A2.
XX
PD 07-FEB-2002.
XX
PF 28-AUG-2001; 2001WO-EP09892.
XX
PR 28-AUG-2001; 2001WO-EP09892.

XX (FARB) BAYER AG.
XX
XX Tietjen K, Weidler M;
XX WPI; 2002-269010/31.
DR
XX
PT Identifying plant target proteins for herbicidally active compounds,
PT comprising aligning and comparing nucleic acid or amino acid sequences
PT from plant with nucleic acid or amino acid sequences from non-plant
PT organisms -
XX
PS Claim 5; SEQ ID NO 2259; 261pp + Sequence Listing; English.
XX
CC The invention relates to identifying target proteins
CC (ABB90790-ABB94016) for herbicidally active compounds, comprising
CC aligning and comparing nucleic acid or amino acid sequences from plant
CC with nucleic acid or amino acid sequences from non-plant organisms using
CC suitable search parameters, where plant sequences having an E-value
CC greater by a factor of 3 than the E-value of most similar non-plant
CC sequences are selected. The polypeptides or nucleic acids encoding them
CC are useful for identifying modulators. The identified modulators are
CC useful as herbicides.
XX
SQ Sequence 335 AA;
Query Match 94.3%; Score 1739; DB 23; Length 335;
Best Local Similarity 95.2%; Pred. No. 1.4e-190;
Matches 334; Conservative 1; Mismatches 0; Indels 16; Gaps 1;
QY 1 MAATGSSGTLTISRPLVTLRRSRAAVSYSSSHRLLHLLPLSSRLLLNHRVQATIL 60
DB 1 MAATGSSGTLTISRPLVTLRRSRAAVSYSSSHRLLHLLPLSSRLLLNHRVQATIL 60
QY 61 QDDEKVVVEESFKAETSTGTPELEPNMSSSTSAFETWIIKLEQGVNVLTDVSVIKIL 120
DB 61 QDDEKVVVEESFKAETSTGTPELEPNMSSSTSAFETWIIKLEQGVNVLTDVSVIKIL 120
QY 121 DTLYRDRTYARFFVLETIARVPYFAFMSVLHMYETFGWRRADYLVKVFHFAESWNEHHLL 180
DB 121 DTLYRDRTYARFFVLETIARVPYFAFMSVLHMYETFGWRRADYLVKVFHFAESWNEHHLL 180
QY 181 IMEELGNSWDFRFLAQHIAFYFMTVFLYILSPRMAYHFSECVESHAYETYDKFLKA 240
DB 181 IMEELGNSWDFRFLAQHIAFYFMTVFLYILSPRMAYHFSECVESHAYETYDKFLKA 240
QY 241 SGEELKNMPADIAVKYTTGGDLYLDFEQTSTRTPTNTRRPVNIENLYDVFNIRDDAEHC 300
DB 241 SGEELKNMPADIAVKYTTGGDLYLDFEQTSTRTPTNTRRPVNIENLYDVFNIRDDAEHC 300
QY 301 KTRACOTLGSLRSPHSIILDDDDTEESGCVVPEEAHCEGIVDCLKKSITS 351
DB 285 KTRACOTLGSLRSPHSIILDDDDTEESGCVVPEEAHCEGIVDCLKKSITS 335
RESULT 3
AAG22097
ID AAG22097 standard; Protein; 318 AA.
XX
AC AAG22097;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24896.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX

PD 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
PF XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
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XX AC AAG46350;
XX DT 18-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 58303.
DE Arabidopsis thaliana
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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XX	SO	Sequence	329 AA;
		Query Match	10.2%; Score 187.5; DB 23; Length 329;
		Best Local Similarity	25.5%; Pred. No. 2.2e-12;
		Matches	60; Conservative 40; Mismatches 90; Indels 45; Gaps 7;
Qy	71	ESFKAETSTGTEPLEEPNMSSSSTSAFETWIKLEOGVNVFLTDSVIKILDTLDRRTYA	130
Db	107	ETYRADL---TIDLKHHVPSTLPDKIAYMWVK-----SLRWPTDLFFQRYYGC	152
Qy	131	RFFVLETIARVPYFAFMSVLHM-----YETFGWMRRADYLKVHFAESWNEMHHLLIMEEL	185
Db	153	RAIMLETVAAPGVGMGLMHFKSLRFEOSGGW-----TKALLEEAENRMHLMTFMEV	207
Qy	186	GGNSWFEDRFIAQHIAFYFYFMVTFLYILSPRMAYHFSECVSHAYETDYDKFLK-ASGEE	244
Db	208	-AKPKWVERALVISVOGFNAYLVIGLIISPKFAHRMVGYLEEAIHSYTEFLKELDNGN	266
Qy	245	LKNPAPDIAVKYTTGGDLYLFDEFOFSRTPNTRRPVNIENLYDVFNIRDEAEH	299
Db	267	IENVPAPIADVW-----RLPADATLRDVMVMVRADAAH	302
		RESULT 13	
ID	ABB91225	standard; Protein; 287 AA.	
XX	AC	ABB91225;	
XX	DT	31-MAY-2002 (first entry)	
XX	DE	Herbicidally active polypeptide SEQ ID NO 436.	
XX	KW	Herbicidal; plant; agriculture; herbicide.	
XX	OS	Arabidopsis thaliana.	
XX	PN	WO200210210-A2.	
XX	PD	07-FEB-2002.	
XX	PF	28-AUG-2001; 2001WO-EP09892.	
XX	PR	28-AUG-2001; 2001WO-EP09892.	
PA	(FARB)	BAYER AG.	
XX	PI	Tietjen K, Weidler M;	
XX	DR	WPI; 2002-269010/31.	
XX	PT	Identifying plant target proteins for herbicidally active compounds,	
XX	PT	comprising aligning and comparing nucleic acid or amino acid sequences	
XX	PT	from plants with nucleic acid or amino acid sequences from non-plant	
XX	PS	organisms -	
XX	Claim 5;	SEQ ID NO 436; 261pp + Sequence Listing; English.	
CC	The invention relates to identifying target proteins		
CC	(ABB90790-ABB94016) for herbicidally active compounds, comprising		
CC	aligning and comparing nucleic acid or amino acid sequences from plant		
CC	with nucleic acid or amino acid sequences from non-plant organisms using		
CC	suitable search parameters, where plant sequences having an E-value		
CC	greater by a factor of 3 than the E-value of most similar non-plant		
CC	sequences are selected. The polypeptides or nucleic acids encoding them		
CC	are useful for identifying modulators. The identified modulators are		
XX	useful as herbicides.		
XX	Sequence	287 AA;	
	Query Match	10.1%; Score 187; DB 23; Length 287;	
	Best Local Similarity	26.2%; Pred. No. 2.1e-12;	

Matches	80; Conservative	47; Mismatches	102; Indels	76; Gaps	1
Qy	16	RPLV--TLRRSRAAVSYSSHRLHLHPSSRLL-----LRNNHRVQAATILQDDDEEK	66		
Db	11	RPLVSSVSOLGIGGFRGH-LISHLP--NVRLLSSDTSPPVSGNQNPENPIRTAD-GK	66		
Qy	67	VVVESFKAETSTGTEP--LEEPNMSSSSTSAFETWIKLEOGVNVFLTDSVIKILDITLY	124		
Db	67	VI-----STYWGIPPTKITKPDGSAMKNCQFPW-----DSYKPDYSI-----	104		
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Qy	236	KELK-ASGEELKNMPADIAVKYTTGGDLYLFDEFOFSRTPNTRRPVNIENLYDVFNIR	294		
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KW	Protein identification; signal transduction pathway; metabolic pathway;				
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XX	termination sequence..				
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Db 178 RAMMLETVAAPGVMGMLLHCKSLRRFEQSGW----IKALLEEAENERMHLMTFMEV 232
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Search completed: February 2, 2003, 22:45:34
Job time : 76 secs
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COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/863,169A
FILING DATE: 03-APR-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/822,011
FILING DATE: 19-JAN-1992
CLASSIFICATION: 530
APPLICATION NUMBER: US 07/937,893
FILING DATE: 18-APR-1991
CLASSIFICATION: 530
APPLICATION NUMBER: US 615,715
FILING DATE: 20-NOV-1990
CLASSIFICATION: 530
APPLICATION NUMBER: US 510,706
FILING DATE: 18-APR-1990
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:297/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-863-169A-5

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RESULT 7

US-08-424-268-8
Sequence 8, Application US/08424268
Patent No. 5821118
GENERAL INFORMATION:
APPLICANT: Omer, Charles A
APPLICANT: Diehl, Ronald E
APPLICANT: Gibbs, Jackson B
APPLICANT: Kohl, Nancy E
TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein
TRANSFERASE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Metck & Co., Inc.
STREET: P.O.Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Power Mac
OPERATING SYSTEM: System 7.5.3
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,268
FILING DATE: 4/24/95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18858PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3903
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
US-08-424-268-8

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; GENERAL INFORMATION:
; APPLICANT:
; SEQUENCE CHARACTERISTICS: BROWN, MICHAEL S.
; SEQUENCE CHARACTERISTICS: GOLDSTEIN, JOSEPH L.
; SEQUENCE CHARACTERISTICS: REISS, YUVAL
; SEQUENCE CHARACTERISTICS: MARSTERS, JR., JAMES C.
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; ADDRESSEE: CHARACTERIZATION AND
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; COUNTRY: UNITED STATES OF AMERICA
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; FILING DATE: 24 AUGUST 1992 (24.08.92)
; NAME: UNKNOWN
; ATTORNEY/AGENT INFORMATION:
; APPLICATION NUMBER: PCT/US93/10442
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; REFERENCE/DOCKET NUMBER: UTFD377PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 512-474-7577
; TELEX: NOT APPLICABLE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US93-08062-5

Query Match
Best Local Similarity 4.5%; Score 82.5; DB 5; Length 379;
Matches 70; Conservative 67; Mismatches 137; Indels 105; Gaps 17;

QY 2 AAISGSSGTLTISRPLVTLRRSRA-----AVSYSSSHRLHLHLPLSSRLLLRNHRV 55
Db 46 AVASPMDDGFSVLDSPSYVLYRDRAEWADIDVPQNDGPNPVQIIYSK---FRDVIDY 102
QY 56 QATILQDDEKVVVEESPKAETSTGTPELEPNMSSSTSAFETWIK-----LEQGVNV 110
Db 103 FRVLQDERS---ERAFKL-----TRDAIELNAANYTVMHFRVLLKSLQKDLHEEMN- 153
QY 111 FLTDSVIKILDTLYRDTYARFV-----LETIARVPYFAPMSVLHM-YETFGWR 160
Db 154 YIT-ALIEQPKNYQVWHRRVLEWLRDPSQLEFIA-----DILNQDAKNYHAWQ 204
QY 161 RADYLVKVFHFAESNMHHL--LIMEELGNSWDFRFLAQHIAFYFMTVFLYLSPRM 218
Db 205 HRQWVIOEFKLDNELQVYDQLLKEDVRNNSVMNQRY-----FVISNTT 248
QY 219 AYHFSECVESHAYETYDKELKASGEELKNMPADIAVYYTGGDLYLDFDEQTSRTPNTR 278
Db 249 GYNDRAVLEREVOYTL-----EMIKLVPHNESAWNYLKG---ILQDRGLSKYPNLL 296
QY 279 RPVIE-----NLYDFVFNIRDEAEH-----CKTMRACOTLG----- 310
Db 297 NQLLDLQPSHSPYLLIAFLVDIYEDMLENQCNKEDILNKALELCEILAKEKDTIRKEYW 356
QY 311 -----SLRSPHSILDDDDT 324
Db 357 RYIGRSLQSKHSTENDSPT 375

RESULT 11
PCT-US93-10442-8
; Sequence 8, Application PC/TUS9310442
; GENERAL INFORMATION:
; APPLICANT: Omer, Charles A
; APPLICANT: Diehl, Ronald E
; APPLICANT: Gibbs, Jackson B
; APPLICANT: Kohl, Nancy E
; TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein
; TRANSFERASE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O.Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10442
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; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/968,782
; FILING DATE: 10/30/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Muthard, David A
; REGISTRATION NUMBER: 35,297
; REFERENCE/DOCKET NUMBER: 18858
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3903
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
;
PCT-US93-10442-8

Query Match 4.5%; Score 82.5; DB 5; Length 379;
Best Local Similarity 18.5%; Pred. No. 0.76;
Matches 70; Conservative 67; Mismatches 137; Indels 105; Gaps 17;

QY 2 AAISGSSGTLTISRPLVTLRRSRA-----AVSYSSSHRLLHLLPLSSRLLRNHRV 55
Db 46 AVASPMDDGFVSLDSPSYVLYRDAEWADIDVPONDGPNPVQIYISDK---FRDVIDY 102
QY 56 QATILQDDEKVVVEESFKAETSTGTEPLEPNMSSSTSAFETWIK-----LEQGVNV 110
Db 103 FRVLQDERS---ERAFKL-----TRDAIELNAANYVWHRFVLLKSLQKDLHEEN- 153
QY 111 FLTDSVIKILDTLYRDRTYARFV-----LETIARVPYFAFMSVLHM-YETFGWR 160
Db 154 YIT-AITIEOPKQNVQVWHRRLVLEWLRDPSQLEFIA-----DILNODAKNYHAWQ 204
QY 161 RADYLVKVFSAESNMHHL--LIMEELGNSWDFRFLAQHIATFYFMTVFLYLSPRM 218
Db 205 HRQWVIOEFKLDNELOYVDQLLKEDVRNNSVWQRY-----FVISNTT 248
QY 219 AYHSECVESHAYETYDKFLKASGEELKNMPADIAVYVTGGDLYLDFEFTQSRTPNTR 278
Db 249 GYNDRAVLEREVQYTL-----EMIKLVPHNESAWNYLKG---ILQDRGLSKYPNLL 296
QY 279 RPVIE-----NLYDFVFNIRDEAEH-----CKTMRACQTLG----- 310
Db 297 NOLLDLQPSHSPYLIATFLVDIYEDMLENQCDNKEDILNKALELCEILAKEDTIRKEW 356
QY 311 -----SLRSPHSITLDDDDT 324
Db 357 RYIGRSLOSKHSTENDSPT 375

RESULT 12
US-08-424-268-20
; Sequence 20, Application US/08424268
; Patent No. 5821118
; GENERAL INFORMATION:
; APPLICANT: Omer, Charles A
; APPLICANT: Diehl, Ronald E
; APPLICANT: Gibbs, Jackson B
; APPLICANT: Kohl, Nancy E
; TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P O Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
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; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Power Mac
; OPERATING SYSTEM: System 7.5.3
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,268
; FILING DATE: 4/24/95
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muthard, David A
; REGISTRATION NUMBER: 35,297
; REFERENCE/DOCKET NUMBER: 18858PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3903
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 819 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
;
US-08-424-268-20

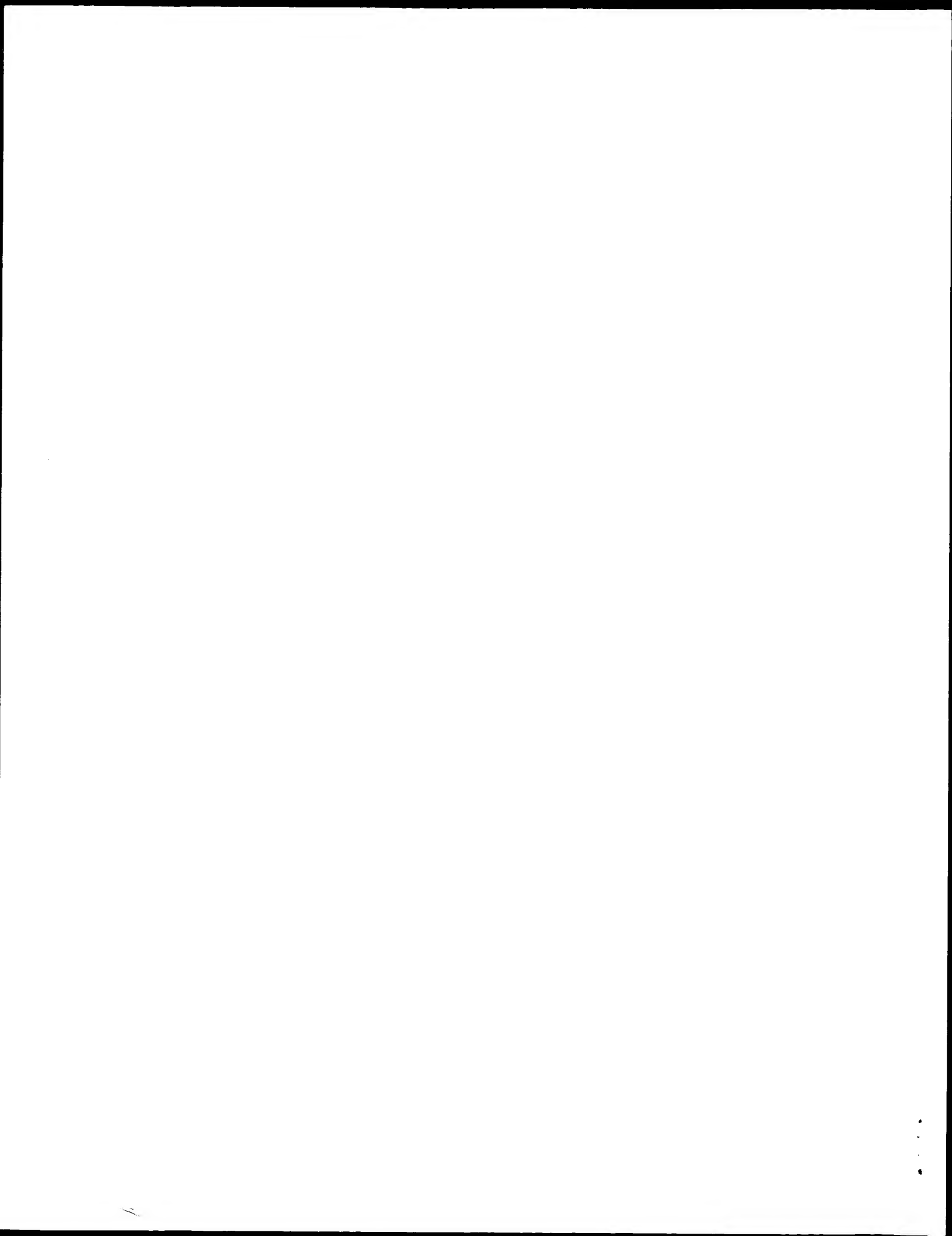
Query Match 4.5%; Score 82.5; DB 2; Length 819;
Best Local Similarity 18.5%; Pred. No. 2.7;
Matches 70; Conservative 67; Mismatches 137; Indels 105; Gaps 17;

QY 2 AAISGSSGTLTISRPLVTLRRSRA-----AVSYSSSHRLLHLLPLSSRLLRNHRV 55
Db 486 AVASPMDDGFVSLDSPSYVLYRDAEWADIDVPONDGPNPVQIYISDK---FRDVIDY 542
QY 56 QATILQDDEKVVVEESFKAETSTGTEPLEPNMSSSTSAFETWIK-----LEQGVNV 110
Db 543 FRVLQDERS---ERAFKL-----TRDAIELNAANYVWHRFVLLKSLQKDLHEEN- 593
QY 111 FLTDSVIKILDTLYRDRTYARFV-----LETIARVPYFAFMSVLHM-YETFGWR 160
Db 594 YIT-AITIEOPKQNVQVWHRRLVLEWLRDPSQLEFIA-----DILNODAKNYHAWQ 644
QY 161 RADYLVKVFSAESNMHHL--LIMEELGNSWDFRFLAQHIATFYFMTVFLYLSPRM 218
Db 645 HRQWVIOEFKLDNELOYVDQLLKEDVRNNSVWQRY-----FVISNTT 688
QY 219 AYHSECVESHAYETYDKFLKASGEELKNMPADIAVYVTGGDLYLDFEFTQSRTPNTR 278
Db 689 GYNDRAVLEREVQYTL-----EMIKLVPHNESAWNYLKG---ILQDRGLSKYPNLL 736
QY 279 RPVIE-----NLYDFVFNIRDEAEH-----CKTMRACQTLG----- 310
Db 737 NOLLDLQPSHSPYLIATFLVDIYEDMLENQCDNKEDILNKALELCEILAKEDTIRKEW 796
QY 311 -----SLRSPHSITLDDDDT 324
Db 797 RYIGRSLOSKHSTENDSPT 815

RESULT 13
PCT-US93-10442-20
; Sequence 20, Application PC/TUS9310442
; GENERAL INFORMATION:
; APPLICANT: Omer, Charles A
; APPLICANT: Diehl, Ronald E
; APPLICANT: Gibbs, Jackson B
; APPLICANT: Kohl, Nancy E
; TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P O Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
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Db 79 LLIQNLHRI-----DPEGKXHVAFIENLLRQIGTRSPTEVEICTKPEILFTLMAGYE 132
Qy 99 TW--IIKLEQGVNVLTDVSIKILDTLYRDTVAREFVLETIARVPVFAFMSVLHMYETF 156
Db 133 DAHPEIALNSGTML-----RECARY---EALAKI-----MLHSDEFF 166
Qy 157 GWRRRADYLVHFA-----ESWNEM---HLLIMEELGGSWDFDRFLAQAHIATFYFMTV 209
Db 167 KFRVVEVSTFDIASDAFSTFKELLTRKLLCAEFLDAN---YDKFFSQ----- 212
Qy 210 FLYILSPRMAYHFSECVEHAYETYDKELKASGEELKNMPADIAVXYTGGD-LYL--- 265
Db 213 -----HYQRLNSENIVTRQSLKLLGELLDRHNTVMTRYISEPENLKLMMN 261
Qy 266 -----FDEFQTSR---TENTRRPVIE-----NLYDVFNIRDEAE 298
Db 262 MLKEKSRNIQFEAPHVFKVFNANPKPKPILDLILRNQTKLVDELTFNFTDRSE 315

Search completed: February 2, 2003, 22:49:18
Job time : 28 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 2, 2003, 22:46:20 ; Search time 18 Seconds
(without alignments)
393.482 Million cell updates/sec

Title: US-09-807-867-2

Perfect score: 1845

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_applications_AA.*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB_PEP.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB_PEP.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB_PEP.*
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- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB_PEP.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	96	5.2	917	10	US-09-815-242-5603
2	96	5.2	920	10	US-09-815-242-12181
3	96	5.2	920	10	US-09-815-242-12995
4	96	5.2	920	10	US-09-815-242-13148
5	84.5	4.6	1881	9	US-09-998-425-3
6	82.5	4.5	394	10	US-09-925-302-722
7	80.5	4.4	608	9	US-10-023-437-41
8	80.5	4.4	2139	10	US-09-727-384-6
9	80	4.3	599	10	US-09-952-013A-4
10	79.5	4.3	183	10	US-09-801-574-70
11	78.5	4.3	1167	10	US-09-815-242-11522
12	78	4.2	572	9	US-10-025-222A-39
13	78	4.2	902	9	US-09-922-199A-2
14	77.5	4.2	377	10	US-09-935-390A-31
15	77	4.2	458	10	US-09-742-582-11
16	75.5	4.1	217	10	US-09-841-132-403
17	75.5	4.1	396	10	US-09-925-297-629
18	75.5	4.1	876	9	US-09-712-363-243
19	75	4.1	231	9	US-09-738-626-6594

20	75	4.1	328	9	US-10-028-072-34	Sequence 34, Appl
21	75	4.1	356	9	US-10-120-319-12	Sequence 12, Appl
22	75	4.1	418	9	US-09-832-659-42	Sequence 42, Appl
23	75	4.1	450	9	US-09-738-626-3752	Sequence 3752, Ap
24	74.5	4.0	755	9	US-09-738-626-4773	Sequence 4773, Ap
25	74.5	4.0	941	9	US-09-992-598-353	Sequence 353, App
26	74.5	4.0	941	9	US-09-989-293A-353	Sequence 353, App
27	74.5	4.0	941	9	US-09-989-735-353	Sequence 353, App
28	74.5	4.0	941	9	US-09-990-444-353	Sequence 353, App
29	74.5	4.0	941	9	US-09-989-730-353	Sequence 353, App
30	74.5	4.0	941	9	US-09-990-436-353	Sequence 353, App
31	74.5	4.0	941	9	US-09-991-181-353	Sequence 353, App
32	74.5	4.0	941	9	US-09-993-687-353	Sequence 353, App
33	74.5	4.0	941	9	US-09-989-734-353	Sequence 353, App
34	74.5	4.0	941	9	US-10-028-072-464	Sequence 464, App
35	74.5	4.0	941	9	US-09-997-653-353	Sequence 353, App
36	74.5	4.0	941	10	US-09-989-723-353	Sequence 353, App
37	74.5	4.0	941	10	US-09-989-723-353	Sequence 353, App
38	74.5	4.0	941	10	US-09-989-279-353	Sequence 353, App
39	74.5	4.0	941	10	US-09-989-727-353	Sequence 353, App
40	74.5	4.0	941	10	US-09-989-731-353	Sequence 353, App
41	74.5	4.0	941	10	US-09-989-732-353	Sequence 353, App
42	74.5	4.0	941	10	US-09-991-073-353	Sequence 353, App
43	74.5	4.0	941	10	US-09-990-442-353	Sequence 353, App
44	74.5	4.0	941	10	US-09-991-163-353	Sequence 353, App
45	74.5	4.0	941	10	US-09-993-604-353	Sequence 353, App

ALIGNMENTS

RESULT 1
US-09-815-242-5603
; Sequence 5603, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: PASTSEQ for Windows Version 4.0
; SEQ ID NO 5603
; LENGTH: 917
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-5603

Query Match 5.2%; Score 96; DB 10; Length 917;
Best Local Similarity 19.8%; Pred. No. 0.28;

Matches 67; **Conservative** 44; **Mismatches** 122; **Indels** 106; **Gaps** 13;

QY	71	ESPKAETSTGTEPLEPENMSSSSTSAFETWIKLEGVNVFLTDSVIKILDTPLYRD-RTY	129
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QY	130	AREF-----VLET-----IARPPYFAFMSVLHMVYETFGWRRADYLVK	167
Db	652	LRFMGLNIDNPDTSIPESSELLEVDRYLLNRLREET-ASTINNYENF-----DYLNI	704
QY	168	HFAESNEMHLLIME-----ELGNSWNF---DRFLAQHTATFYFMTVFLYILSPRM	218
Db	705	-----TOEVQNFINVLSNFYLDYGKDLIYIEQORDSHIRSMQTVLYQLVDMTKLLAPI	759
QY	219	AYHFSECVESHAYETYDKFLKASGEELKNMPADIAPKYVYTGDDLYLFEDEFOTSRTPNTR	278
Db	760	LVHTAEVWSHT-----PHVKESVHLADMPK-----VVEVDQALLDKWRT-----	800
QY	279	RPVLIENLYDVFNIRDEAEHCKTMR-----ACQTLGSLRSHP	316
Db	801	-----FMRLRDVNRVALETARNEKVICSLKAKVTIASNDKFNASEFLTDFDALH	850
QY	317	SI-----LDDDDTEBSGCVVPEAHCEGIVDC	344
Db	851	QLFIVSQVKVWDLDDQATAYEHGDIVIEHAGEKCERC	889

RESULT 2

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US-09-815-242-12181
; Sequence 12181, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12181
; LENGTH: 920
; TYPE: PRN
; ORGANISM: Staphylococcus aureus
US-09-815-242-12181

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Query Match 5.2%; Score 96; DB 10; Length 920;
Best Local Similarity 19.8%; Pred. No. 0.28;
Matches 67; Conservative 44; Mismatches 122; Indels 106; Gaps 13;

QY 71 ESFKAETGTGTEPLEEPMSSSTSAFTWIKLEGVNVFLTDSVKILDTLRD-RTY 129

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RESULT 3

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RES001.3
US-09-815-242-12995
; Sequence 12995, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12995
; LENGTH: 920
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-12995

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Query Match          5.2%; Score 96; DB 10; Length 920;
Best Local Similarity 19.8%; Pred. No. 0.28;
Matches 67; Conservative 44; Mismatches 122; Indels 106; Gaps 13;

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| | | | | : : : : : | : : : : | : | : | : | : | : | : |
595 EGKMKSKSLGNVVPDQVQKQKQKADIAFLWSSDYLADYRISDEILKQTSDFYRKIRNT 654

DB
| | | | | : : : : : | : : : : | : | : | : | : | : | : |
QY 130 ARFF-----VLET---IARVPYFAFMSVLHMYETFGWRRADYLVK 167
| | | | | : : : : : | : : : : | : | : | : | : | : | : |

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Db 655 LRFMLGNINDFNPDTSIPESSELLEVDYRLNRLREFT-ASTINNYENF-----DYLNI 707
QY 168 HFAESWNEHHLLIME-----ELGNSWVF---DRFLAQHIATFYFMTVFLYLSRPM 218
Db 708 -----YQEVQNFINVLSNFYLDYKGLDLYTEQDSDSHIRSMQTVLYILVDMTKLLAPI 762
QY 219 AYHFSECVESHAYETYDKFLKASGEELKNMPADIAVKYTYTGGDLYLDFDEFQTSRTPNTR 278
Db 763 LVHTAEVWSHT-----PHVKEESVHLADMPK-----VVEVDQALLDKWRT----- 803
QY 279 RPVIENLYDVFNIRDDAEHCKTMR-----ACQTLGLSLRSPH 316
Db 804 -----FMNLRDDVNRALETARNEKVIKGSLEAKVTIASNDKFNASEFLTSFDALH 853
QY 317 SI-----LDDDDTEESGCVVPEEAHCEGIVDC 344
Db 854 QLFIVSQVKYVDKLDQDQATAYEHGDIVIEHADGECERC 892

RESULT 4

US-09-815-242-13148
; Sequence 13148, Application US/09815242
; Patent No. US2002061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13148
; LENGTH: 920
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-13148

Query Match 5.2%; Score 96; DB 10; Length 920;
Best Local Similarity 19.8%; Pred. No. 0.28;
Matches 67; Conservative 44; Mismatches 122; Indels 106; Gaps 13;

QY 71 ESFKAETSTGTPELEPNMSSSTSAFETWIKLEQGVNVLTDVSVIKILDTLYRD-RTY 129
Db 595 EGKMSKSLGNVIVDPQVVVKQKAGIARLWVSSDTLADVRISDEILKQTSDDVYRKIRNT 654
QY 130 ARFF-----VLET-----TARVPYFAFMSVLHMYETFGWRRADYLVK 167
Db 655 LRFMLGNINDFNPDTSIPESSELLEVDYRLNRLREFT-ASTINNYENF-----DYLNI 707
QY 168 HFAESWNEHHLLIME-----ELGNSWVF---DRFLAQHIATFYFMTVFLYLSRPM 218

Db 708 -----YQEVQNFINVLSNFYLDYKGLDLYTEQDSDSHIRSMQTVLYILVDMTKLLAPI 762
QY 219 AYHFSECVESHAYETYDKFLKASGEELKNMPADIAVKYTYTGGDLYLDFDEFQTSRTPNTR 278
Db 763 LVHTAEVWSHT-----PHVKEESVHLADMPK-----VVEVDQALLDKWRT----- 803
QY 279 RPVIENLYDVFNIRDDAEHCKTMR-----ACQTLGLSLRSPH 316
Db 804 -----FMNLRDDVNRALETARNEKVIKGSLEAKVTIASNDKFNASEFLTSFDALH 853
QY 317 SI-----LDDDDTEESGCVVPEEAHCEGIVDC 344
Db 854 QLFIVSQVKYVDKLDQDQATAYEHGDIVIEHADGECERC 892

RESULT 5

US-09-998-425-3
; Sequence 3, Application US/09998425
; Publication No. US20030008346A1
; GENERAL INFORMATION:
; APPLICANT: Bartel, Paul L.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: MMSC1 - An MMAC1 Interacting Protein
; FILE REFERENCE: MMSC1 Gene
; CURRENT APPLICATION NUMBER: US/09/998,425
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/233,086
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/071,861
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-20
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1881
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-998-425-3

Query Match 4.6%; Score 84.5; DB 9; Length 1881;
Best Local Similarity 22.0%; Pred. No. 11;
Matches 67; Conservative 41; Mismatches 111; Indels 85; Gaps 14;

QY 74 KATSTGTCTEPLPEPNMSSS-----STSAFETWIKLEQGVNVLTDVSVIK-ILDTLYRD 126
Db 451 RKTSSSTSPLEPPSDRGCTVVEPLKPPALFTGAVETE--TNVDGEDEEIKERIDTLKND 508
QY 127 RTYARFTVLETIARVP-----YFAMSVLHMYETFGWRRADYLVKH 168
Db 509 NIQA---LEKLEKVPDSPENELKSRWENLLGPDYEVWVATLDT-----QIADDAELQ 557
QY 169 FAESWNEHHLLIMEELGNSWVFDRFLAQHIATFYFMTVF-----LYILSPRMAYH 221
Db 558 KSKLLPIHTLRIGVEV-----DSFDGHH-----YISSIVSGPVDTLGLLOPE---- 601
QY 222 FSECVESHAYETYDKFLKASGEELKNMPADIAVKYTYTGGDLYLDFDE---FQTSRTPNTR 278
Db 602 -DELLEVNGMLYCKSRREAVSFLKEVPPPTLVCCRR-----LFDDEASVDEPRTEETS 655
QY 279 RPVIENLYDVFNIRDD-----EAEHCKTMRACQTLGLSLRSPHSLDDDDDEETES 328
Db 656 LPETEVDHNDVNTPEDDDGELALWSPEVKIVELVKCKGLG-----FSLDYQDPLDPT 710
QY 329 GCVV 332
Db 711 RSVI 714

RESULT 6

US-09-925-302-722
; Sequence 722, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 722
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-722

Query Match 4.5%; Score 82.5; DB 10; Length 394;
Best Local Similarity 18.5%; Pred. No. 2;
Matches 70; Conservative 67; Mismatches 137; Indels 105; Gaps 17;

QY 2 AALSGSSGFLTISRPLVLRSSRA-----AVSYSSSHRLLHLLPLSSRRLLRNHRV 55
DB 61 AVASPMDDGFVLDSPSYLYDRAEWADIDVPQDGNPVVQIYSDK---FRDVYDY 117
QY 56 QATVLODEKVVVEESFKAETSTGTEPLEEPNMSSSTSAFETWIK-----LEQGVNV 110
DB 118 FRAVLQORDERS---ERAFKL-----TRDAIELNAANYTWHFRRVLLKSLQKDLHEEMN- 168
QY 111 FLTDSVIKILDTLRDRTVAREFV-----LETIARVPYFAPMSVLHM-YETFGWNR 160
DB 169 YIT-AIEEPKNQYQVWHRRVLEWLRDPDSOELEFIA-----DILNDAKNYHAWQ 219
QY 161 RADYLVKVFHAESNMHHL--LIMEPLGNSWNWDFRFLAQHIATFYFMTVFLYILSPRM 218
DB 220 HRCWVTOEKLWNLQYDQDLKEDVRNNSVWQRY-----FVLSNTT 263
QY 219 AYHFSCEVSHAYETYDKFLKASGEELKNMPADIAVYITGGDLYLDFEFTSRTPNTR 278
DB 264 GYNDAVLEREQVYTL-----EMIKLVPHNESAWNLYKG---ILQDRGLSKYPNLL 311
QY 279 RPVIE-----NLVDVFNVRDDEAEH-----CKTWRACQTLG----- 310
DB 312 NQLLDQPSHSPPIAFVLDIYEDMLENQCDNKEDILNKALELCEILAKEKDTIRKEYW 371
QY 311 -----SLRPSHSLDDDDT 324
DB 372 RYIGRSLQSKHSTENDSPT 390

RESULT 7
US-10-023-437-41
; Sequence 41, Application US/10023437
; Publication No. US2002018372A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEMKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBOECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING NUCLEIC ACID
; FILE REFERENCE: US/023,437
; CURRENT APPLICATION NUMBER: US/10/023,437
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/225,839
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 41
; LENGTH: 608
; TYPE: PRT
; ORGANISM: Chlamydia psittaci
US-10-023-437-41

Query Match 4.4%; Score 80.5; DB 9; Length 608;
Best Local Similarity 25.0%; Pred. No. 5.8;
Matches 44; Conservative 22; Mismatches 77; Indels 33; Gaps 6;
QY 73 FKAETSTGTEPLEEPNMSSSTSAFETWIKLEQGVNVFLTDSVIKILDTLRDRTYAR 131
DB 425 FLAETASTLNEMLLMSMLKESDSK-----EEKITI-LTRCLDTIFSTLFR----- 469
QY 132 FVLETTIARVPYFAPMSVLHMYETFGWNRADYLVKVFHAESNMHHLIMEELGGNSW 191
DB 470 -----QVLFASEFYDIHAAEHGVPLTEYLSSTYKKNLQNEFYGEIITFDVLSIEW 521
QY 192 FDRFLAQHIATFYFMTVFLYILSPRMAYHSECV---ESHAYETYDKFLKASGEE 244
DB 522 -----ARIPHFYFNFYVYATGIIAALCFLEKILNEDNALNSYLNFLKSGSD 571

RESULT 8
US-09-727-384-6
; Sequence 6, Application US/09727384
; Patent No. US2002009851A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Heichman, Karen
; APPLICANT: Cimborra, Daniel M.
; APPLICANT: Bush, Angie
; APPLICANT: Mauck, Kimberly
; APPLICANT: Bartel, Paul L.

; TITLE OF INVENTION: Protein-Protein Interactions
; FILE REFERENCE: 2318-271
; CURRENT APPLICATION NUMBER: US/09/727,384
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/168,377
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: US 60/168,379
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: US 60/185,056
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 6
; LENGTH: 2139
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-727-384-6

Query Match 4.4%; Score 80.5; DB 10; Length 2139;
Best Local Similarity 24.8%; Pred. No. 35;
Matches 51; Conservative 22; Mismatches 58; Indels 75; Gaps 12;

QY 157 GWRERADYLVKVFHAESNMHHLIMEELG---GNSWDFRFLAQHIATFYFMTVFLYI 213
DB 30 GFHRKIOHVK-----NELCHMLSLFEVAPVLOQTLLQDLNLLGR--VHFDQKEALILI 80
QY 214 LSPRMA--YHFSCEVSHAYETYDKFLKASGEELKNMPADIAV---KYITGGDLY--- 264
DB 81 LSRTLSNEEFHQE-----PDCSLEAQPXKVRGKRYGRR 114
QY 265 LDFEFTSRTPNTRFVNIENLYDVFNVRDDEA-----EHCKTMRA--CQTLGS 311
DB 115 SLFEFQESVEEFPEVTVIEPL-----DEEARPSHIPAGDCSEHWKTORSEYEAEQ 166
QY 312 LR--SPHSILDDDDTEESGCVVPEE 335
DB 167 LRFWNP-----DOLNASQSGSPFPQD 187

RESULT 9
US-09-952-013A-4
; Sequence 4, Application US/09952013A
; Patent No. US2002014680A1
; GENERAL INFORMATION:

```
; APPLICANT: GRUMMT, Ingrid
; APPLICANT: VINGRON, Martin
; TITLE OF INVENTION: RNA POLYMERASE I TRANSCRIPTION FACTOR TIF-1A
; FILE REFERENCE: 38485-0007
; CURRENT APPLICATION NUMBER: US/09/952.013A
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: PCT/DE00/00767
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: DE 199 11 992.9
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-09-952-013A-4

Query Match      4.3%; Score 80; DB 10; Length 599;
Best Local Similarity 18.9%; Pred. No. 6.4;
Matches 68; Conservative 56; Mismatches 97; Indels 138; Gaps 18;

QY 7 ISSGTLTISRPLTLRRSRAVSVSSHRLHLPLSSRRLLRNHRVQATILQ----- 61
DB 17 VNGTMSSTNVPD--RTVGSKFSSA-----VSKNDGRLMQOMLRAFAVVK 60
QY 62 -DDE-----EKVVVESEFKAETGTGTEPLEEPNMSSTSAFETWIKLEQGVNVF 111
DB 61 ALDDKAEGNFAGYEDLRQFAKSDTKDAPSSLOQLNLSALT-----CNVS 107
QY 112 LTDS-----VIKILDTLY--RD-----RTYARF-----FVLETIARVPYFAFMSVLHMYETFG 157
DB 108 RLDSSNLSVMSVLDVWVSDESFVRCYTRFLGNLSAQSNYLPVMTMLIQHML----- 163
QY 158 WMRADYLKVHFAESWNEHHLLIMEELGNSWDFRPLAOHIAFFYFMTVFVLIISPR 217
DB 164 --YRPDSLAIHYEHA-----HMAKXVLELV-----PR 189
QY 218 M-AVHFSECVSHAVETYDKELKASGEELKNPAPDIATVYKTTGGDLYLDFEFTSRTPN 276
DB 190 AHUSFLYSILIEFPYK--DESLLAQMTYISNV-----LSICEY-----VPS 228
QY 277 TRRPVNIENLYDVFNIRDEAEHCCKTRACQTLGLRSPHSILDDDDTEESGCVWPEE 335
DB 229 IKGVPVLAIDKIIQI-DVEIQ-----VEVDDDDDEEDEVVTD 267

RESULT 10
US-09-801-574-70
; Sequence 70, Application US/09801574
; Patent No. US20020081592A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Peifeng Jeremy
; APPLICANT: Page, David C.
; TITLE OF INVENTION: Reproduction-Specific Genes
; FILE REFERENCE: 0399.2007-002
; CURRENT APPLICATION NUMBER: US/09/801.574
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: 60/187,518
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: 60/261,557
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-574-70

Query Match      4.3%; Score 79.5; DB 10; Length 183;
Best Local Similarity 35.5%; Pred. No. 1.3;
Matches 33; Conservative 9; Mismatches 9; Indels 15; Gaps 6;
```

```
QY 253 IAVKYVTGGDLYLDFEFTSRTPNTRRPVNIENLYDVFNIRDEAEHC--KTRACQTLGS 311
DB 25 ITLELYT-SYLYLSMAFYFNRDD-----VALENFFRYFLRLSDDKMEHAQKLMR-----LQN 75
QY 312 LRSPHSILDDDDTEE-----ESGCVWPEEA-HCE 339
DB 76 LRGGHICLHDIRKPECGQWESGLVAMESAFHLE 108

RESULT 11
US-09-815-242-11522
; Sequence 11522, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815.242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11522
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-815-242-11522
```

```
Query Match      4.3%; Score 78.5; DB 10; Length 1167;
Best Local Similarity 18.1%; Pred. No. 24;
Matches 59; Conservative 49; Mismatches 111; Indels 107; Gaps 11;

QY 40 LPLSSRRLLRN-NHRVQATILQD-----DE-----EKVVVESEFKAETS 78
DB 172 LPALRESEIKNLDEAVKNTNFONINKVLKALRSHDSSLVDDEAFKEKTKIFGSDASNP 231
QY 79 TGTEPLEEPNMSSTSAFETWIKLEQGVNVFLTDSVLIKILDTLYRDTYARFVLETI 138
DB 232 DDEEELQKDKTEQSSNDPKQAQTLFDAILLODLANAVYVMPTKLGDRNYWENFAKKT- 290
QY 139 ARVPYAFMSVLHMYETFGWRRADYLKVHFAESWNEHHLLIMEELGNSWDFRFLA- 197
DB 291 -----GNIARTLNER-----LKEFGKNPELFDNPLTS 318
QY 198 -----OHIAIFYFYFMTVFVLIISPRMAYHFSECVSHAYETYDKEL 238
DB 319 LRGNHQSIKEERALDMLISHIIT-----KPIFDAIFGDNKFNPIAKALDKMWLKLSDGL 374
QY 239 KASGEELKNMPAPDIATVYKTTGGDLYLDFEFTQ-----SRTPNTRRPVNIENLYDVFNIR 294
DB 375 EGKTKDLKN-----LYESVKTEAARAKSKQSQOELIKNLYNTFFK---- 414
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OM protein - protein search, using sw model
Run on: February 2, 2003, 22:44:50 ; Search time 40 seconds
(without alignments)
843.580 Million cell updates/sec

Title: US-09-807-867-2
Perfect score: 1845
Sequence: 1 MAATSGTSSGTLTISRPLVT.....VPEAHCEGIVDCLKKSITS 351

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73: *
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1841	99.8	351	2 T52422	alternative oxidas
2	1739	94.3	335	2 T04907	hypothetical prote
3	721	39.1	230	2 AB2068	oxidase [imported]
4	208	11.3	333	2 T08850	alternative respir
5	200.5	10.9	274	2 S45035	alternative respir
6	198.5	10.8	353	2 T04094	alternative respir
7	197.5	10.7	297	2 S51278	alternative respir
8	194.5	10.5	318	2 C86448	hypothetical prote
9	193	10.5	321	2 S31711	alternative respir
10	190.5	10.3	326	2 T08849	alternative respir
11	190	10.3	353	2 T07805	alternative oxidas
12	185.5	10.1	305	2 A46364	alternative respir
13	185.5	10.1	353	2 T51615	alternative respir
14	169.5	9.2	349	2 T30143	alternative respir
15	169.5	9.2	349	2 A39158	alternative respir
16	161.5	8.8	149	2 T01433	alternative respir
17	153.5	8.3	342	2 S17517	alternative oxidas
18	141.5	7.7	362	2 S65752	alternative oxidas
19	128	6.9	339	2 T07947	alternative prote
20	104	5.6	721	2 T05815	hypothetical prote
21	103.5	5.6	1920	2 A53188	pericentrin - mous
22	100	5.4	444	2 T13155	linoleoyl-CoA desa
23	100	5.4	3255	2 G81702	adherence factor T
24	99	5.4	345	2 T09018	probable calcium-b
25	98.5	5.3	2265	2 T26183	hypothetical prote
26	98	5.3	435	2 H90578	conserved hypothet
27	96	5.2	917	2 S40178	isoleucine-tRNA li
28	96	5.2	917	2 D89891	Ile-tRNA synthetas
29	93.5	5.1	2693	2 A40743	IP3 receptor, XIP3

30	93	5.0	1174	2 H84982	exodeoxyribonuclea
31	92.5	5.0	394	2 E81286	probable polysacch
32	91	4.9	736	1 VPXRPC	outer layer protei
33	91	4.9	853	2 H69172	DNA helicase II re
34	91	4.9	1422	2 T24212	hypothetical prote
35	90	4.9	361	2 B90461	hypothetical prote
36	89.5	4.9	979	2 JH0109	glycoprotein 14 pr
37	88.5	4.8	773	2 T39513	hypothetical prote
38	88.5	4.8	967	2 S28428	phosphoenolpyruvat
39	88	4.8	409	2 D96912	o-acetylhomoserine
40	88	4.8	444	2 JG0180	Delta6 fatty acid
41	88	4.8	921	2 H69643	isoleucine-tRNA li
42	88	4.8	1482	2 T34010	hypothetical prote
43	87.5	4.7	437	2 E71290	probable flagellar
44	87.5	4.7	618	2 T39100	hypothetical prote
45	87.5	4.7	702	2 A61619	arylphorin precurs

ALIGNMENTS

RESULT 1

T52422
alternative oxidase-related protein IMMUTANS [validated] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 24-Oct-2000
C:Accession: T52422
R:Wu, D.; Wright, D.A.; Wetzel, C.; Voytas, D.F.; Rodermel, S.R.
Plant Cell 11, 43-55, 1999
A:Title: The IMMUTANS variegation locus of Arabidopsis defines a mitochondrial altern
A:Reference number: Z26073; MUID:99096708; PMID:9878631
A:Accession: T52422
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-351 <WUD>
A:Cross-references: EMBL:AF098072; PIDN:AAD03599.1
C:Genetics:
A:Gene: IM
A:Map position: IV
C:Function:
A:Description: Involved in nuclear gene induced variegation of arabidopsis leaves [va
for phytoene desaturation

Query Match 99.8%; Score 1841; DB 2: Length 351;
Best Local Similarity 99.7%; Pred. No 1.2e-156;
Matches 350; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAATSGTSSGTLTISRPLVTLRKRAAVSYSSSHRLHLHLPLSSRLLLRNNHRVQATIL	60
DB	1	MAATSGTSSGTLTISRPLVTLRKRAAVSYSSSHRLHLHLPLSSRLLLRNNHRVQATIL	60
QY	61	QDDEKVVVVESEFKAETSTGTETLEPNMSSSTSAFETWIKLEQGVNVLDTSVIKIL	120
DB	61	QDDEKVVVVESEFKAETSTGTETLEPNMSSSTSAFETWIKLEQGVNVLDTSVIKIL	120
QY	121	DTLYRDTYARFFVLETIARVPYAFMSVLHMVETFGWRRADYLVKVFHFAESNMHHLL	180
DB	121	DTLYRDTYARFFVLETIARVPYAFMSVLHMVETFGWRRADYLVKVFHFAESNMHHLL	180
QY	181	IMEELGNSWDFRFLAQHIATFYFMTVFLYILSPRMAYHFSECVSHAYETYDKFLKA	240
DB	181	IMEELGNSWDFRFLAQHIATFYFMTVFLYILSPRMAYHFSECVSHAYETYDKFLKA	240
QY	241	SGEELKNWAPDTAVKYTGGDLYLDFEFOTSRTPNTRRPVNIENLYDFVNIIRDDAEHC	300
DB	241	SGEELKNWAPDTAVKYTGGDLYLDFEFOTSRTPNTRRPVNIENLYDFVNIIRDDAEHC	300
QY	301	KTMACOTGLSLRSPHSLDDDDTEESGCVVPEAHCEGIVDCLKKSITS	351
DB	301	KTMACOTGLSLRSPHSLDDDDTEESGCVVPEAHCEGIVDCLKKSITS	351

RESULT 2

T04907
hypothetical protein T10114.90 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
C:Accession: T04907
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.
submitted to the Protein Sequence Database, April 1998
A:Reference number: Z15389
A:Map position: 4
A:Introns: 50/2; 113/3; 145/1; 183/3; 220/1; 243/1; 267/1
A:Note: T10114.90

Query Match 94.3%; Score 1739; DB 2; Length 335;
Best Local Similarity 95.2%; Pred. No. 1.5e-147;
Matches 334; Conservative 1; Mismatches 0; Indels 16; Gaps 1;

QY 1 MAAGISSGTTISPLVTLRRSAAVSYSSSHRLHLPLSSRRLLRNHRVOATIL 60
|||||
Db 1 MAAGISSGTTISPLVTLRRSAAVSYSSSHRLHLPLSSRRLLRNHRVOATIL 60
|||||

QY 61 QDDEKVVVEESFKATSTGTGTEPLEEPNMSSSTSAFETWIKLEQGVNVLTDVSKIL 120
|||||
Db 61 QDDEKVVVEESFKATSTGTGTEPLEEPNMSSSTSAFETWIKLEQGVNVLTDVSKIL 120
|||||

QY 121 DTLYRDTYARFVLETIARVPYFAPMSVLHMYETFGWWRADYLVKVFHAFSWNEMHLL 180
|||||
Db 121 DTLYRDTYARFVLETIARVPYFAPMSVLHMYETFGWWRADYLVKVFHAFSWNEMHLL 180
|||||

QY 181 IMEELGNSWDFRFLAQHIAFYFMTVFLXILSPRAYHFSECVSHAYETVDKFLKA 240
|||||
Db 181 IMEELGNSWDFRFLAQHIAFYFMTVFLXILSPRAYHFSECVSHAYETVDKFLKA 240
|||||

QY 241 SGEELKNMPADIAKYTGGLDYLDFDEQTSRTPTNTRPVNIENLYDVFNIRDEAEHC 300
|||||
Db 241 SGEELKNMPADIAKYTGGLDYLDFDEQTSRTPTNTRPVNIENLYDVFNIRDEAEHC 300
|||||

QY 301 KTMRCOTLGLSRSPHSILDDDTTEESGCVVPEAHCEGIVDCLKKSITS 351
|||||
Db 285 KTMRCOTLGLSRSPHSILDDDTTEESGCVVPEAHCEGIVDCLKKSITS 335
|||||

RESULT 3
AB2068
oxidase [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: AB2068
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriiguchi, H.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AB2068
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-230 <CUR>
A:Cross-references: GB:BA000019; PIDN:BAB73795.1; PID:g17131187; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all2096

Query Match 39.1%; Score 721; DB 2; Length 230;
Best Local Similarity 60.0%; Pred. No. 8.4e-57;
Matches 132; Conservative 34; Mismatches 44; Indels 10; Gaps 12;

QY 101 IIKLEQGVNVLTDVSKILDTLYRDTYARFVLETIARVPYFAPMSVLHMYETFGWR 160

Db 1 MIRLLVGLVLF-----VINTVYDRPYPRFYVLETVARVPVFSYLSLHLVETLGGWR 53
QY 161 RADYLVKVFHAFSWNEMHLLIMEELGNSWDFRFLAQHIAFYFMTVFLXILSPRAYH 220
Db 54 KADYLVKVFHAFSWNEMHLLIMEELGNSWDFRFLAQHIAFYFMTVFLXILSPRAYH 113
QY 221 HFSECVSHAYETVDKFLKASGEELKNMPADIAKYTGGLDYLDFDEQTSRTPTNTR 280
Db 114 NFMEOVEQAHAYSSYDKFLTTHEAEKLTQPAPEVAKTYIRGDLVMEDEFQTAHSPSPRRP 173
QY 281 VIENLYDVFNIRDEAEHCCTMRACOTLG---SLRSPHS 317
Db 174 NIDNLYDVFNIRDEAEHCCTMRACOTLG---SLRSPHS 213

RESULT 4
T08850
alternative respiratory pathway oxidase (EC 1.-.-) Aox2 - soybean
C:Species: Glycine max (soybean)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 12-Nov-1999
C:Accession: T08850
R:Finnegan, P.M.; Whelan, J.; Millar, A.H.; Zhang, Q.; Smith, M.K.; Wiskich, J.T.; Da
Plant Physiol. 118, 675-682, 1998
A:Title: Differential expression of the multigene family encoding the soybean mitochon
A:Reference number: Z16494
A:Accession: T08850
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-333 <FIN>
A:Cross-references: EMBL:U07906; NID:g2769671; PID:g1946336
C:Genetics:
A:Note: Aox2
C:Superfamily: alternative oxidase
C:Keywords: oxidoreductase

Query Match 11.3%; Score 208; DB 2; Length 333;
Best Local Similarity 28.5%; Pred. No. 9.8e-11;
Matches 74; Conservative 35; Mismatches 95; Indels 56; Gaps 10;

QY 65 EKVVEESF-----KAETSTGTEPLEEPNMSSSTSAFETWIKLEQGVNVLTDVSKIL 113
Db 78 EKVVEESF-----KAETSTGTEPLEEPNMSSSTSAFETWIKLEQGVNVLTDVSKIL 127
QY 114 ----DSV-----IKIL-----DTLYRDTYARFVLETIARVPYFAPMSVLHMYETFGWR 161
Db 128 KNVLDKVAYRTVKLLRPTDFFKRRYGCRAAMLEITVAAPGVGMVGGMLHLRLSRKFQOS 187
QY 162 ADYLVKVFHAFSWNEMHLLIMEELGNSWDFRFLAQHIAFYFMTVFLXILSPRAYH 221
Db 188 GWTIKALLEEAENRHLMTMVEL-VKPKWYERLLVLAVQGVFFNAFFVLYILSPKVAHR 246
QY 222 FSECVSHAYETVDKFLK--ASGEELKNMPADIAKYTGGLDYLDFDEQTSRTPTNTR 279
Db 247 IVGLEEEAHSYTEYKLDLESG-AIENVPAPAIADYW-----RL 286
QY 280 PVNIENLYDVFNIRDEAEH 299
Db 287 PKDARLKDVITVIRADEAHH 306

RESULT 5
S45035
alternative respiratory pathway oxidase (EC 1.-.-) AOMI - mango
C:Species: Mangifera indica (mango)
A:Variety: cv. Manila
C:Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 19-May-2000
C:Accession: S45035
R:Cruz-Hernandez, A.; Gomez-Lim, M.A.
submitted to the EMBL Data Library, May 1994
A:Description: Molecular cloning and expression studies of the alternative oxidase fr
A:Reference number: S45035
A:Accession: S45035


```

QY      295 DEAH 299
      ||| I
Db      290 DEAH 294

RESULT 10
T08849
alternative respiratory pathway oxidase (EC 1.-.-.) Aox3 - soybean
C:Species: Glycine max (soybean)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 12-Nov-1999
C:Accession: T08849
R:Finnegan, P.M.; Whelan, J.; Millar, A.H.; Zhang, Q.; Smith, M.K.; Wiskich, J.T.; Da
Plant Physiol. 118, 675-682, 1998
A:Title: Differential expression of the multigene family encoding the soybean mitocho
A:Reference number: Z16494
A:Accession: T08849
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-326 <FIN>
A:Cross-references: EMBL:U87907; NID:g1946337; PID:g1946338
C:Genetics:
A:Gene: Aox3
C:Superfamily: alternative oxidase
C:Keywords: oxidoreductase

Query Match      10.3%; Score 190.5; DB 2; Length 326;
Best Local Similarity 32.8%; Pred. No. 3.5e-09;
Matches 66; Conservative 27; Mismatches 71; Indels 37; Gaps 9;

QY      112 LTVDSV-----IKIL----DTLYRDTYARFFVLETIARVPYFAFMSVLHMYETFGWRRAD 163
      ||| I      :| I      :| I      :| I      :| I      :| I      :
Db      123 LTKVAPRAVKELRVLSDIVFKERYGCHAMMLETIAAPGVMGMLLHLKSLRKFOHSGG 182
      ||| I      :| I      :| I      :| I      :| I      :| I      :

QY      164 YLKVHFAESNEMHHLLIMEELGNSWFR---FLAQHIATFYFTVFLYILSPMAY 220
      :| I      :| I      :| I      :| I      :| I      :| I      :| I      :|
Db      183 WIKALLEEAENRMHLMTMVELVKPS-WHERLLIFTAQGV--FFNAFFVF-YLLSPKAAH 238
      :| I      :| I      :| I      :| I      :| I      :| I      :| I      :

QY      221 HFSECVSHAYERYDPLKA--SGEELKNPAPDIAVKYVTGGDLYLDFDEFQTSRTPTNR 278
      :| I      :| I      :| I      :| I      :| I      :| I      :| I      :
Db      239 RFVCLLEEAAVISYTOHNLNIESG-KVENVPAPALDIYW-----R 278
      :| I      :| I      :| I      :| I      :| I      :| I      :| I      :

QY      279 RPVIENLYDFVNIIRDDEAH 299
      :| I      :| I      :| I      :| I      :| I      :| I      :
Db      279 LPKDATLKDVTVIRADEAHH 299
      :| I      :| I      :| I      :| I      :| I      :| I      :

RESULT 11
T07805
alternative oxidase (EC 1.-.-.) - Madagascar periwinkle
C:Species: Catharanthus roseus (Madagascar periwinkle)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C:Accession: T07805
R:Kiyota, S.
submitted to the EMBL Data Library, December 1997
A:Description: cDNA of alternative oxidase from Catharanthus roseus culture cells.
A:Reference number: Z16144
A:Accession: T07805
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-353 <KIY>
A:Cross-references: EMBL:AB009395
C:Genetics:
A:Genome: nuclear
C:Function:
A:Description: catalyzes cyanide-resistant oxygen consumption
C:Superfamily: alternative oxidase
C:Keywords: membrane protein; mitochondrial inner membrane; mitochondrion; oxidoreduc

Query Match      10.3%; Score 190; DB 2; Length 353;
Best Local Similarity 23.5%; Pred. No. 4.3e-09;
Matches 84; Conservative 53; Mismatches 124; Indels 96; Gaps 15;

QY      7 ISSGTLTIRPLVTLRRRAAVSYSSSHLLHHLPL-----SSRR-146

```

A:Reference number: 225414
A:Accession: T51615
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-353 <LAC>
A:Cross-references: EMBL:AJ131392; PIDN:CAA10364.1
A:Experimental source: cultivar ecotype Columbia
C:Genetics:
A:Gene: hsr3
A:Note: expressed during hypersensitive response of Arabidopsis thaliana to the bacterium
C:Superfamily: alternative oxidase
C:Keywords: oxidoreductase

Query Match 10.1%; Score 185.5; DB 2; Length 353;
Best Local Similarity 25.1%; Pred. No. 1.1e-08;
Matches 59; Conservative 41; Mismatches 90; Indels 45; Gaps 7;

QY 71 ESFKAETSTGTEPLEEPNMSSTSAFETWIKLEQGVNVLDTSDVVKILDTLYRDRTYA 130
Db 131 ETYKADI---TIDLKHHVPTTFLDRIAYTVK-----SLRWPTDLFFQRRYGC 176
QY 131 RFFVLETIARVPYFAPMSVLH-----MYETFGWRRADYLVKHFASWNEHMLIMEEL 185
Db 177 RAMLETVAAPVGMVGMGLLHCKSLRRFEQSGW-----IKALLEAEENRMLHMTFMEV 231
QY 186 GGNWFWDFRFLAQHIATFYFMTVFLYILSPRMAYHFSECVESHAYETDYKFLKASGE-E 244
Db 232 -AKPKWYERALVITVQGVFFENAYFLGLISPKFAHRMVGYLEEETHSYTEFLKELDKGN 290
QY 245 LKNMPPADIAVKYTGDDLYLDFEFQTSRTPNTRRPVNIENLYDVFNIRDEAEH 299
Db 291 IENVPAPATAIDYW-----RLPADATLRDVMVVRADAAH 326

RESULT 14
S30143
A:Title: alternative respiratory pathway oxidase (EC 1.1.3.-) - voodoo lily
C:Species: Sauromatum guttatum (voodoo lily)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Sep-1999
C:Accession: S30143
R:Roads: D.M.; McIntosh, L.
Plant Mol. Biol. 21, 615-624, 1993
A:Title: The salicylic acid-inducible alternative oxidase gene axo1 and genes encoding
A:Reference number: S30143; MUID:93192522; PMID:8448361
A:Accession: S30143
A:Molecule type: DNA
A:Residues: 1-349 <RHO>
A:Cross-references: EMBL:Z15117; NID:g21215; PIDN:CAA70823.1; PID:g21216
C:Genetics:
A:Gene: axo1
A:Introns: 124/3; 167/3; 330/3
C:Superfamily: alternative oxidase
C:Keywords: membrane protein; mitochondrial inner membrane; mitochondrion; oxidoreductase

Query Match 9.2%; Score 169.5; DB 2; Length 349;
Best Local Similarity 28.1%; Pred. No. 2.9e-07;
Matches 52; Conservative 27; Mismatches 75; Indels 31; Gaps 5;

QY 121 DTLYRDRTYARFFVLETIARVPYFAPMSVLH-----MYETFGWRRADYLVKHFASWNE 175
Db 163 DIFFORRYACRAMLETVAAPVGMVGMGLLHCKSLRRFEHSGGWIRA-----LLEAEAE 217
QY 176 MHULLIMEELGNSWDFRFLAQHIATFYFMTVFLYILSPRMAYHFSECVESHAYETDY 235
Db 218 RMHLMTFMEV-AOPRWYERALVAVOGVFFENAYFLGLISPKFAHRMVGYLEEETHSYT 276
QY 236 KFLK-ASGEELKNNPAPDIAVKYTGDDLYLDFEFQTSRTPNTRRPVNIENLYDVFNIR 294
Db 277 EFLKIDONGAIOQCPAPATAIDYW-----RLPADATLRDVMVVRADAAH 326

QY 295 DEAEH 299
Db 318 DEAHH 322

Db 2 MSRGATISRSU-----COISPRYFSSAAVRGHEPFLSGILTSGGTTTFLHGNPONGSERT 57
QY 47 -----LLLNRRNRVATLODEEKVVEESFKAETSTGTEP-----LEEPNMSSS 92
Db 58 ALTWIKLPMRARSASTVATVDQDKDEKDKNGVADGNGKAVSYWGVAPKATKE 117
QY 93 S-----TSAFETW-----IILKEQGVNVLDTSDV-----IKIL-----DTLYRDRTYAR 131
Db 118 DCTVNRWTCFRPWETPKDPTDIELKHHVPVTLDDKVAFFTVKALRPDTPDLFFQRRYGC 177
QY 132 FVLETIARVPYFAPMSVLH-----MYETFGWRRADYLVKHFASWNEHMLIMEELG 186
Db 178 AMLETVAAPVGMVGMGLLHCKSLRRFEHSGW-----IKALLEAEENRMLHMTFMEV- 231
QY 187 GNSWFWDFR---FLAQHIATFYFMTVFLYILSPRMAYHFSECVESHAYETDYKFLKASGE 243
Db 232 SKPRWTERALFVAVOGVFFENAYFLT---YLASPKLHAIRIVGYLEEEAHSYSEFLNELDK 288
QY 244 -ELKNMPPADIAVKYTGDDLYLDFEFQTSRTPNTRRPVNIENLYDVFNIRDEAEH 299
Db 289 GNIENVPAPATAIDYW-----QMPDSTLRDVMVVRADAAH 326

RESULT 12
A46364
A:Title: alternative respiratory pathway oxidase (EC 1.1.3.-) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999
C:Accession: A46364
R:Kumar, A.M.; Soll, D.
Proc. Natl. Acad. Sci. U.S.A. 89, 10842-10846, 1992
A:Title: Arabidopsis alternative oxidase sustains Escherichia coli respiration.
A:Reference number: A46364; MUID:93066339; PMID:1438286
A:Accession: A46364
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-305 <KUM>
A:Cross-references: GB:M96417; NID:g166875; PIDN:AAA32870.1; PID:g166876
A:Note: sequence extracted from NCBI backbone (NCBIP:118704)
C:Superfamily: alternative oxidase
C:Keywords: membrane protein; mitochondrial inner membrane; mitochondrion; oxidoreductase

Query Match 10.1%; Score 185.5; DB 2; Length 305;
Best Local Similarity 25.1%; Pred. No. 8.9e-09;
Matches 59; Conservative 41; Mismatches 90; Indels 45; Gaps 7;

QY 71 ESFKAETSTGTEPLEEPNMSSTSAFETWIKLEQGVNVLDTSDVVKILDTLYRDRTYA 130
Db 83 ETYKADI---TIDLKHHVPTTFLDRIAYTVK-----SLRWPTDLFFQRRYGC 128
QY 131 RFFVLETIARVPYFAPMSVLH-----MYETFGWRRADYLVKHFASWNEHMLIMEEL 185
Db 129 RAMLETVAAPVGMVGMGLLHCKSLRRFEQSGW-----IKALLEAEENRMLHMTFMEV 183
QY 186 GGNWFWDFRFLAQHIATFYFMTVFLYILSPRMAYHFSECVESHAYETDYKFLKASGE-E 244
Db 184 -AKPKWYERALVITVQGVFFENAYFLGLISPKFAHRMVGYLEEETHSYTEFLKELDKGN 242
QY 245 LKNMPPADIAVKYTGDDLYLDFEFQTSRTPNTRRPVNIENLYDVFNIRDEAEH 299
Db 243 IENVPAPATAIDYW-----RLPADATLRDVMVVRADAAH 278

RESULT 13
T51615
A:Title: alternative respiratory pathway oxidase (EC 1.1.3.-) [similarity] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C:Accession: T51615
R:Lacomme, C.J.; Roby, D.
FEBS Lett. 459, 149-153, 1999
A:Title: Identification of new early markers of the hypersensitive response in Arabidopsis

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OM protein - protein search, using sw model

Run On: February 2, 2003, 22:07:45 ; Search time 22 Seconds

(without alignments)
661.736 Million cell updates/sec

Title: US-09-807-867-2

Perfect score: 1845

Sequence: 1 MAATGSSGTLTISRPLVT.....VPEAHCEGIVDCLKRSITS 351

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	208	11.3	333	1 AOX2_SOYBN	041266 glycine max
2	200.5	10.9	297	1 AOX2_TOBAC	Q40578 nicotiana t
3	200.5	10.9	318	1 AOX1_MANIN	Q40294 mangifera i
4	196.5	10.8	353	1 AOX1_TOBAC	Q41224 nicotiana t
5	194.5	10.5	353	1 AOX2_ARATH	Q22049 arabidopsis
6	190.5	10.3	326	1 AOX3_SOYBN	Q03376 glycine max
7	189	10.2	321	1 AOX1_SOYBN	Q07185 glycine max
8	187.5	10.2	329	1 AX1C_ARATH	Q22048 arabidopsis
9	185.5	10.1	354	1 AX1A_ARATH	Q39219 arabidopsis
10	176.5	9.6	325	1 AX1B_ARATH	Q23913 arabidopsis
11	169.5	9.2	349	1 AOX1_SAUGU	P22185 saurumatum
12	163	8.8	351	1 AOX_ASPNG	Q74180 aspergillus
13	153.5	8.3	342	1 AOX_HANAN	Q00912 hansenua a
14	141.5	7.7	362	1 AOX_NEUCR	Q01355 neurospora
15	111.5	6.0	345	1 AOX_TRYBB	Q26710 trypanosoma
16	103.5	5.6	1920	1 PCNT_MOUSE	P48725 mus musculus
17	101.5	5.5	326	1 HEM2_PASMU	P57874 pasteurella
18	96	5.2	917	1 SY1_STAAU	P41972 staphylococ
19	93.5	5.1	916	1 SCRB_LIMPO	Q25386 limulus pol
20	93	5.0	1174	1 EX5B_BUCAI	P57529 buchnera ap
21	91	4.9	736	1 VP4_ROTFC	P26193 porcine rot
22	90	4.9	624	1 PSAB_AMPCA	P58383 amphidinium
23	89.5	4.9	979	1 VGLB_HSVEL	P25218 equine herp
24	88.5	4.8	967	1 CAP1_SOYBN	Q02909 glycine max
25	88	4.8	921	1 SY1_BACSU	Q45477 bacillus su
26	87.5	4.7	437	1 FLHE_TREPA	Q56339 treponema p
27	87.5	4.7	653	1 MTSL_STRSA	P29347 streptococ
28	87.5	4.7	980	1 VGLB_HSVEL	P18551 equine herp
29	87.5	4.7	980	1 VGLB_HSVEL	P28922 equine herp
30	87	4.7	590	1 PEPF_BORBU	O51264 borrelia bu
31	87	4.7	956	1 SY1_AQUAE	O66651 aquifex aeo
32	86.5	4.7	980	1 VGLB_HSVEL	P18050 equine herp
33	86	4.7	272	1 CAT5_YEAST	P41735 saccharomyc

34	85.5	4.6	2131	1 YCF2_SPIOL	P08973 spinacia ol
35	85	4.6	633	1 NOF1_DROME	P15296 drosophila
36	85	4.6	960	1 CAP2_SORBI	P29194 sorghum bic
37	85	4.6	960	1 CAP3_SORBI	P15804 sorghum bic
38	85	4.6	966	1 CAP1_MESCR	P10490 mesembryant
39	85	4.6	967	1 CAP2_MAIZE	P51059 zea mays (m
40	85	4.6	984	1 NOF_DROME	P16320 drosophila
41	84.5	4.6	1165	1 SYV_AQUAE	O67411 aquifex aeo
42	84	4.6	323	1 HEMZ_HAEIN	P43868 haemophilus
43	84	4.6	377	1 APJ_RAT	Q9Jing3 ratus norv
44	84	4.6	687	1 YBGO_YEAST	P34225 saccharomyc
45	83.5	4.5	356	1 YD6E_SCHPO	Q10323 schizosacch

ALIGNMENTS

```

RESULT 1
AOX2_SOYBN
ID AOX2_SOYBN STANDARD; PRT; 333 AA.
AC Q41266;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alternative oxidase 2, mitochondrial precursor (EC 1.-.-.-).
GN AOX2.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP MEDLINE-97336308; PubMed-9193084;
RA Finnegan P.M., Whelan J., Millar A.H., Zhang Q., Smith M.K.,
RA Wiskich J.T., Day D.A.;
RT "Differential expression of the multigene family encoding the soybean
RT mitochondrial alternative oxidase.";
RL Plant Physiol. 114:455-466(1997).
RN [2]
SEQUENCE OF 206-245 FROM N.A.
RX MEDLINE-96165778; PubMed-8580775;
RA Whelan J., Millar A.H., Day D.A.;
RT "The alternative oxidase is encoded in a multigene family in
RT soybean.";
RL Planta 198:197-201(1996).
CC -!- FUNCTION: CATALYZES CYANIDE-RESISTANT OXYGEN CONSUMPTION. MAY
CC INCREASE RESPIRATION WHEN THE CYTOCHROME RESPIRATORY PATHWAY IS
CC RESTRICTED, OR IN RESPONSE TO LOW TEMPERATURES (BY SIMILARITY).
CC -!- PATHWAY: Alternative respiratory pathway.
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (PROBABLE).
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL, POSSIBLY IN THE INNER SURFACE
CC OF THE INNER MITOCHONDRIAL MEMBRANE.
CC -!- SIMILARITY: BELONGS TO THE ALTERNATIVE OXIDASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U87906; AAB97285.1; -
CC EMBL: S81470; AAB36072.1; -
CC InterPro: IPR002680; AOX.
CC Pfam: PF01786; AOX; 1.
CC Oxidoreductase; Transit peptide; Mitochondrion; Respiratory chain;
CC Inner membrane; Transmembrane; Multigene family.
CC TRANSIT 1 ? 333 MITOCHONDRION (POTENTIAL).
CC CHAIN ? 333 ALTERNATIVE OXIDASE 2.
CC TRANSMEM 158 178 POTENTIAL.
CC TRANSMEM 220 240

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FT DISULFID 106 106 INTERCHAIN (POTENTIAL).
FT METAL 124 124 POTENTIAL.
FT METAL 177 177 POTENTIAL.
FT METAL 204 204 POTENTIAL.
FT METAL 245 245 POTENTIAL.
FT METAL 306 306 POTENTIAL.
FT METAL 311 311 POTENTIAL.
SQ SEQUENCE 333 AA; 38128 MW; 40F651E474EBB752 CRC64;

Query Match 11.3%; Score 208; DB 1; Length 333;
Best Local Similarity 28.5%; Pred. No. 4.4e-10;
Matches 74; Conservative 35; Mismatches 95; Indels 56; Gaps 10;

QY 65 EKVVEESF-----KAEITGCTGTEPLEPNSSSTSAFETWIKLQGVNVLFT----- 113
DB 78 EKVVEESYWGISRPKVVDGTE-----WPWCFMPW-ESYRSNVSIDLTQKHVP 127
QY 114 ----DSV-----IKIL-----DTLYRDRYARFVLETIARVYFAFMSVLHMYETFGWRR 161
DB 128 KNLVDKVAVRTVKLLRIPTDLFFKRRYGCRAAMLETVAAVPGMVGMLLHLRLSRKFKQS 187
QY 162 ADYLKVFHAESENMHLLIMEELGGNSWDFRFLAQHIATFYFVMTVLYILSPRMAYH 221
DB 188 GGIWIKALLEEAENRNMHLMITWEL-VRPKWYERLLVLAVQGVFFNAFVYILSPKVAHR 246
QY 222 FSECVESHAYETYDKFLK--ASGEELKNMPADIAVKYITGGDLYLDFEQTSTRTPTNR 279
DB 247 IVGYLEEAHISYTYLKDLESG-AIENVPAPATAIDW-----RL 286
QY 280 PVIENLYDFVNIIRDEAEH 299
DB 287 PKDARLKDQVITVIRADEAHH 306

RESULT 2
ID AOX2_TOBAC STANDARD; PRT; 297 AA.
AC Q40578;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alternative oxidase 2, mitochondrial precursor (EC 1.-.-.-).
GN AOX2.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. SRL;
RX MEDLINE=95288378; PubMed=7770539;
RA Whelan J., Smith M.K., Meijer M., Yu J.W., Badger M.R.,
RA Price G.D., Day D.A.;
RT "Cloning of an additional cDNA for the alternative oxidase in
RT tobacco.";
RL Plant Physiol. 107:1469-1470(1995).
CC -!- FUNCTION: CATALYZES CYANIDE-RESISTANT OXYGEN CONSUMPTION. MAY
CC INCREASE RESPIRATION WHEN THE CYTOCHROME RESPIRATORY PATHWAY IS
CC RESTRICTED, OR IN RESPONSE TO LOW TEMPERATURES (BY SIMILARITY).
CC -!- PATHWAY: Alternative respiratory pathway.
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (PROBABLE).
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL, POSSIBLY IN THE INNER SURFACE
CC OF THE INNER MITOCHONDRIAL MEMBRANE.
CC -!- SIMILARITY: BELONGS TO THE ALTERNATIVE OXIDASE FAMILY.
CC -----
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CC -----
DR EMBL; X79768; CAA56163.1; -.
DR InterPro; IPR002680; AOX.
DR Pfam; PF01786; AOX; 1.
KW Oxidoreductase; Transit peptide; Mitochondrion; Respiratory chain;
FT CHAIN ? 297 MITOCHONDRION (POTENTIAL).
FT TRANSIT 1 ? ALTERNATIVE OXIDASE 2.
FT CHAIN ? 297 MITOCHONDRION (POTENTIAL).
FT TRANSMEM 184 204 POTENTIAL.
FT DISULFID 70 70 INTERCHAIN (POTENTIAL).
FT METAL 88 88 POTENTIAL.
FT METAL 141 141 POTENTIAL.
FT METAL 168 168 POTENTIAL.
FT METAL 209 209 POTENTIAL.
FT METAL 270 270 POTENTIAL.
FT METAL 275 275 POTENTIAL.
FT UNSURE 209 209
SQ SEQUENCE 297 AA; 33843 MW; 659DBC58E88917E1 CRC64;

Query Match 10.9%; Score 200.5; DB 1; Length 297;
Best Local Similarity 27.2%; Pred. No. 1.6e-09;
Matches 65; Conservative 40; Mismatches 81; Indels 53; Gaps 10;

QY 71 ESFKAETSTGTGLEPNSSSTSAFETWIK-LEQGVNVLFTSVIKILDTLYDRDY 129
DB 75 ETYKADLSI---DLTKHAPTTFLDKFAYTVKALRYPTDIF-----FQRRYG 119
QY 130 ARFFVLETIARVYFAFMSVLH-----MYETFGWRRADYLVHFAESNMHLLIMEE 184
DB 120 CRAMMLETVAAVPGMVGMLLCKLSLRFEQSGW-----IKALLEEAENRNMHLMITME 174
QY 185 LGGNSWDFR---FLAQHIATFYFVMTVLYILSPRMAYHSECVESHAYETYDKFLKAS 241
DB 175 VAKPN-WYERALLVFAVQGVFINAYFVT---YLLSPKLARIYGVYLEEAHISYTFELKEL 230
QY 242 GE-ELKNMPADIAVKYITGGDLYLDFEQTSTRTPTNRPIENLYDFVNIIRDEAEH 299
DB 231 DKGNIENVPAPATAIDW-----RLPKDSTLRDVLVVRADAEAH 270

RESULT 3
AOXL_MANIN STANDARD; PRT; 318 AA.
AC Q40294;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alternative oxidase, mitochondrial precursor (EC 1.-.-.-).
GN AOMI 1.
OS Mangifera indica (Mango).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids II; Sapindales; Anacardiaceae; Mangifera.
OX NCBI_TaxID=29780;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Manila.
RX MEDLINE=96137185; PubMed=8555961;
RA Cruz-Hernandez A., Gomez-Lim M.A.;
RT "Alternative oxidase from mango (Mangifera indica, L.) is
RT differentially regulated during fruit ripening.";
RL Planta 197:569-576(1995).
CC -!- FUNCTION: CATALYZES CYANIDE-RESISTANT OXYGEN CONSUMPTION. MAY
CC INCREASE RESPIRATION WHEN THE CYTOCHROME RESPIRATORY PATHWAY IS
CC RESTRICTED, OR IN RESPONSE TO LOW TEMPERATURES (BY SIMILARITY).
CC -!- PATHWAY: Homodimer; disulfide-linked (PROBABLE).
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (PROBABLE).
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL, POSSIBLY IN THE INNER SURFACE
CC OF THE INNER MITOCHONDRIAL MEMBRANE.
CC -!- INDUCTION: INCREASES DURING RIPENING.
CC -!- SIMILARITY: BELONGS TO THE ALTERNATIVE OXIDASE FAMILY.
CC -----
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Best Local Similarity 25.1%; Pred. No. 3.6e-08;
Matches 59; Conservative 41; Mismatches 90; Indels 45; Gaps 7;

QY 71 ESFKAETSTGTEPLEPNMSSSTSAFETWIKLEQGVNVFLTDSVVIKILDTLYRDRYA 130
Db 132 ETYKADI---TIDLKHHVPTFLDRIAYTVTK-----SLRWPTDLFFQRYGC 177
QY 131 RFFVLETIARVPYFAPMSVLH-----MYETFGWRRADYLVKHFASWNEHHLLIMEEL 185
Db 178 RAMMLETVAAPGVMGMLHCKSLRRFEQSGW-----IKALLEAEANERHMLTMEV 232
QY 186 GNSWFWDFRLAQHIAFYFMTVFLYILSPRMAYHFSECVESHAYETYDKFLK-ASGEE-E 244
Db 233 -AKPKWYERALVITVQGVFNAYFLGLYLSPKFAHRMVGYLEEAEIHSYTEFLKELDKGN 291
QY 245 LKNMPPADIAVYKVTGGDLVLFDEFQTSRTPNTRRPVNIENLYDVFNIRDDAEAH 299
Db 292 IENVPAPAIADYW-----RLPADATLRDVMVVRADAEAH 327

RESULT 10
AX1B.ARATH STANDARD; PRT; 325 AA.
AC Q23913;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alternative oxidase 1b, mitochondrial precursor (EC 1.-.-.-).
GN AOX1B OR AT3G22360 OR MCB17.10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=Leaf, and Stem;
RX MEDLINE=98009993; PubMed=9349280;
RA Saisho D., Nambara E., Naito S., Tsutsumi N., Hirai A., Nakazono M.;
RT "Characterization of the gene family for alternative oxidase from
Arabidopsis thaliana."
RL Plant Mol. Biol. 35:585-596(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20277480; PubMed=10819329;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
features of the regions of 4,504,864 bp covered by sixty P1 and TAC
clones."
RL DNA Res. 7:131-135(2000).
CC -|- FUNCTION: CATALYZES CYANIDE-RESISTANT OXYGEN CONSUMPTION. MAY
INCREASE RESPIRATION WHEN THE CYTOCHROME RESPIRATORY PATHWAY IS
RESTRICTED, OR IN RESPONSE TO LOW TEMPERATURES (BY SIMILARITY).
CC -|- PATHWAY: Alternative respiratory pathway.
CC -|- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (PROBABLE).
CC -|- SUBCELLULAR LOCATION: MITOCHONDRIAL, POSSIBLY IN THE INNER SURFACE
OF THE INNER MITOCHONDRIAL MEMBRANE.
CC -|- SIMILARITY: BELONGS TO THE ALTERNATIVE OXIDASE FAMILY.
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CC -----
DR EMBL; D98875; BAA22624.1; .
DR EMBL; AB022215; BAB01774.1; .
DR InterPro: IPR002680; AOX.
DR Pfam: PF01786; AOX; 1.
KW Oxidoreductase; Transit peptide; Mitochondrion; Respiratory chain;

Inner membrane; Transmembrane: Multigene family.
KW TRANSIT 1 44
FT CHAIN 45 325 MITOCHONDRION (POTENTIAL).
FT TRANSMEM 150 170 ALTERNATIVE OXIDASE 1b.
FT TRANSMEM 212 232 POTENTIAL.
FT DISULFID 98 98 INTERCHAIN (POTENTIAL).
FT METAL 116 116 POTENTIAL.
FT METAL 169 169 POTENTIAL.
FT METAL 196 196 POTENTIAL.
FT METAL 237 237 POTENTIAL.
FT METAL 298 298 POTENTIAL.
FT METAL 303 303 POTENTIAL.
SQ SEQUENCE 325 AA; 37432 MW; 05B0826PDB4A1P2 CRC64;

Query Match 9.6%; Score 176.5; DB 1; Length 325;
Best Local Similarity 24.3%; Pred. No. 1.8e-07;
Matches 57; Conservative 42; Mismatches 91; Indels 45; Gaps 7;

QY 71 ESFKAETSTGTEPLEPNMSSSTSAFETWIKLEQGVNVFLTDSVVIKILDTLYRDRYA 130
Db 103 ETYKSDL--TIDLKHHVPTFLDKLAYTVK-----SLRWPTDLFFQRYGC 148
QY 131 RFFVLETIARVPYFAPMSVLH-----MYETFGWRRADYLVKHFASWNEHHLLIMEEL 185
Db 149 RAMMLETVAAPGVMGMLHCKSLRRFEQSGW-----IKALLEAEANERHMLTMEV 203
QY 186 GNSWFWDFRLAQHIAFYFMTVFLYILSPRMAYHFSECVESHAYETYDKFLK-ASGEE 244
Db 204 AKPN-WYERALVIAVQGIFFNAYFLGLYLSPKFAHRMVGYLEEAEIHSYTEFLKELDKGN 262
QY 245 LKNMPPADIAVYKVTGGDLVLFDEFQTSRTPNTRRPVNIENLYDVFNIRDDAEAH 299
Db 263 IENVPAPAIADYW-----RLPADATLRDVMVVRADAEAH 298

RESULT 11
AOX1.SAUGU STANDARD; PRT; 349 AA.
ID AC P22185;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alternative oxidase, mitochondrial precursor (EC 1.-.-.-).
GN AOX1.
OS Sauromatum guttatum (Voodoo lily).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Sauromatum.
OX NCBI_TaxID=4463;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 67-75.
RX MEDLINE=91172765; PubMed=1706518;
RA Rhoads D.M., McIntosh L.;
RT "Isolation and characterization of a cDNA clone encoding an
alternative oxidase protein of Sauromatum guttatum (Schott).";
RL Proc. Natl. Acad. Sci. U.S.A. 88:2122-2126(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93192522; PubMed=8448361;
RA Rhoads D.M., McIntosh L.;
RT "The salicylic acid-inducible alternative oxidase gene aox1 and genes
encoding pathogenesis-related proteins share regions of sequence
similarity in their promoters."
RL Plant Mol. Biol. 21:615-624(1993).
CC -|- FUNCTION: CATALYZES CYANIDE-RESISTANT OXYGEN CONSUMPTION. MAY
INCREASE RESPIRATION WHEN THE CYTOCHROME RESPIRATORY PATHWAY IS
RESTRICTED, OR IN RESPONSE TO LOW TEMPERATURES. IN S.GUTTATUM THE
ALTERNATIVE RESPIRATORY PATHWAY IS THERMOGENIC.
CC -|- PATHWAY: Alternative respiratory pathway.
CC -|- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (PROBABLE).
CC -|- SUBCELLULAR LOCATION: MITOCHONDRIAL, POSSIBLY IN THE INNER SURFACE
OF THE INNER MITOCHONDRIAL MEMBRANE.
CC -|- INDUCTION: BY SALICYLIC ACID.
CC -|- MISCELLANEOUS: THE 3 ALTERNATIVE OXIDASE PROTEINS DETECTED IN

S. GUTTATUM, WITH APPARENT MW OF 35 kDa, 36 kDa AND 37 kDa, MAY BE POSTTRANSLATIONALLY MODIFIED PRODUCTS OF THE SAME AOX1 GENE.
 -!- SIMILARITY: BELONGS TO THE ALTERNATIVE OXIDASE FAMILY.

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 DR EMBL; M60330; AAA34048.1; -;
 DR EMBL; Z15117; CAA78823.1; ALT_SEQ.
 DR PIR; A39158; A39158.
 DR InterPro; IPR002680; AOX.
 DR Pfam; PF01786; AOX; 1.
 KW Oxidoreductase; Transmembrane; Mitochondrion; Respiratory chain;
 KW Inner membrane; Transmembrane.
 FT TRANSIT 1 63 MITOCHONDRION (POTENTIAL).
 FT CHAIN 64 349 ALTERNATIVE OXIDASE.
 FT TRANSMEM 174 194 POTENTIAL.
 FT TRANSMEM 236 256 POTENTIAL.
 FT DISULFID 122 122 INTERCHAIN (POTENTIAL).
 FT METAL 140 140 POTENTIAL.
 FT METAL 193 193 POTENTIAL.
 FT METAL 220 220 POTENTIAL.
 FT METAL 261 261 POTENTIAL.
 FT METAL 322 322 POTENTIAL.
 FT METAL 327 327 POTENTIAL.
 FT SEQUENCE 349 AA; 38931 MW; 6E70B2B7A858B273 CRC64;

 Query Match 9.2%; Score 169.5; DB 1; Length 349;
 Best Local Similarity 28.1%; Pred. No. 7.6e-07;
 Matches 52; Conservative 27; Mismatches 75; Indels 31; Gaps 5;
 QY 121 DTLYDRRTYARFVLETIARVYFAPMSVLHM-----YETFGWRRADYLKVHFAESWNE 175
 DB 163 DIFFQRRYACRAMLETVAAPGVGVGLHLKSLRFEHSGGWIRA-----LLEEAENE 217
 QY 176 MHLIMEELGNSWMDRFLAQHIATFYFTVFLYILSPRMAYHFSECVESHAYETVD 235
 DB 218 RMHLMTFMEV-AQPRWYERALVAVGVFNAYFLGYLLSPKFAHRVGVYLEEEAIHSIT 276
 QY 236 KFLK-ASGEELKNMPPADIAVKYTGGLYLFDEFQTSRTPTRPVNIENLYDVFVNTRD 294
 DB 277 EPLKDIDSGAIQDCPAPATALDYW-----RLPQGSTLRDVTVVVRA 317
 QY 295 DEAEH 299
 DB 318 DEAHH 322

 RESULT 12
 AOX_ASPNG STANDARD; PRT; 351 AA.
 AC 074180;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alternative oxidase, mitochondrial precursor (EC 1.-.-.-).
 OS AOX1.
 GN Aspergillus niger.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eukotiales; Trichosporaceae; mitosporic Trichosporaceae; Aspergillus.
 OX NCBI_TaxID=5061;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WU-2223L;
 RX MEDLINE=99132188; PubMed=9933359;
 RA Kirmura K., Yoda M., Usami S.;
 RT "Cloning and expression of the cDNA encoding an alternative oxidase
 RT gene from Aspergillus niger WU-2223L.";

Curr. Genet. 34:472-477(1999).
 CC -!- FUNCTION: CATALYZES CYANIDE-RESISTANT OXYGEN CONSUMPTION. MAY
 CC INCREASE RESPIRATION WHEN THE CYTOCHROME RESPIRATORY PATHWAY IS
 CC RESTRICTED, OR IN RESPONSE TO LOW TEMPERATURES (BY SIMILARITY).
 CC -!- PATHWAY: Alternative respiratory pathway.
 CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL, POSSIBLY IN THE INNER SURFACE
 CC OF THE INNER MITOCHONDRIAL MEMBRANE (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE ALTERNATIVE OXIDASE FAMILY.

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 DR EMBL; AB016540; BAA32033.2; -;
 DR InterPro; IPR002680; AOX.
 DR Pfam; PF01786; AOX; 1.
 KW Oxidoreductase; Transmembrane; Mitochondrion; Respiratory chain;
 KW Inner membrane; Transmembrane.
 FT TRANSIT 1 351 MITOCHONDRION (POTENTIAL).
 FT CHAIN 146 166 POTENTIAL.
 FT TRANSMEM 212 232 POTENTIAL.
 FT METAL 98 98 POTENTIAL.
 FT METAL 169 169 POTENTIAL.
 FT METAL 196 196 POTENTIAL.
 FT METAL 237 237 POTENTIAL.
 FT METAL 302 302 POTENTIAL.
 FT METAL 307 307 POTENTIAL.
 FT SEQUENCE 351 AA; 40189 MW; 6307953DF833FD24 CRC64;

 Query Match 8.8%; Score 163; DB 1; Length 351;
 Best Local Similarity 22.3%; Pred. No. 2.7e-06;
 Matches 87; Conservative 61; Mismatches 131; Indels 112; Gaps 19;
 QY 11 TLTISRLVTLRRSRAAVSYSSSHRLHH-----LPLSSRRL--LLRNHRVQATILQDD 63
 DB 3 SLTATAPI-----RAALPKSYMHIATRNYSGVIANSGSLRCSGSIVANRHOTAGKRFIST 56
 QY 64 EEKVVVEESKAEKSTGT-----PLEEPNMSSTSAFETWII-----KL 104
 DB 57 TPKSQIKKEFPPTAPHVKEVETAWHPVYTEQMKGVAIAHRDAKNWADWALGTVMRL 116
 QY 105 EOGYNVFLTDSVIKILDTLYR-----DRTYARFVLETIARVPYAFMS 148
 DB 117 RWGMD-----LVTGYRHPPGREHARFKMTQKWLTRFIFLESVAGVPGWVGGM 166
 QY 149 VLMHYETFGWRRADYLKVHFAESWNEHMLIMEELGNSWMDRFL---AQHIATFY 205
 DB 167 LRHLRLRRMKRNGWLETLEEAYNERMHLTLFLKL-AEPGWFMRLMVLGAQGV---F 221
 QY 206 FMTVFL-YILSPRMAYHFSECVESHAYETVDKFLKASGEELKNMP-----ADIAVKYY 258
 DB 222 FNGFFLSYLSMPRICHREFGVYLEEAVITYTRAIKET--EAGSLPAWEKTEAPEIAVQYW 279
 QY 259 TGGDLYLFDEFQTSRTPTRPVNIENLYDVFVNTRDDAEHCKTMRACOTLGLSLR----- 313
 DB 280 -----KMPEGOR-----SMKDLLLYVRADEAKH---REVNHTLGNLQNAIDP 318
 QY 314 SPHSIDDDDDTEESGCVVPPEAH-CEGIVD 343
 DB 319 NPYAAKYKD-----PTKAHPNKGAD 339

 RESULT 13
 AOX_HANAN STANDARD; PRT; 342 AA.
 ID AOX_HANAN
 AC Q00912;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)

DR	EMBL: U52964; AAB46424.1; -	
DR	InterPro: IPR002680; AOX.	
DR	Pfam: PF01786; AOX, 1	
KW	Oxidoreductase; Transist peptide; Mitochondrion; Respiratory chain;	
KW	Inner membrane; Transmembrane.	
FT	TRANSIT 1	? MITOCHONDRION (POTENTIAL).
FT	CHAIN ?	345 ALTERNATIVE OXIDASE.
FT	TRANSMEM 115	135 POTENTIAL.
FT	TRANSMEM 181	201 POTENTIAL.
FT	DISULFID 95	95 INTERCHAIN (POTENTIAL).
FT	METAL 77	77 POTENTIAL.
FT	METAL 138	138 POTENTIAL.
FT	METAL 165	165 POTENTIAL.
FT	METAL 206	206 POTENTIAL.

Search completed: February 2, 2003, 22:46:11
Job time : 28 secs

Search completed: February 2, 2003, 22:46:11
Job time : 28 secs

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Db 121 DTLVDRRTYARFVLEETIARVYFAFMSVLMHMETFGMMRRADYLKVFHAESENEMHLL 180
QY 181 IMEELGNSMWFDRFLAQHIAITFYMTVFLYLLSPMAVHSECVSHAETTYDKFLKA 240
Db 181 IMEELGNSMWFDRFLAQHIAITFYMTVFLYLLSPMAVHSECVSHAETTYDKFLKA 240
QY 241 SGEELKMPADIAVKYTGDLFLFDEPOTSRTPNTRRPVLENLADVNRDDAEHC 300
Db 241 SGEELKMPADIAVKYTGDLFLFDEPOTSRTPNTRRPVLENLADVNRDDAEHC 300
QY 301 KTRACQTLGSLRSPHSTLDDDDTEESGCVPEEAHCIGIVDCLKKSTIS 351
Db 301 KTRACQTLGSLRSPHSTLDDDDTEESGCVPEEAHCIGIVDCLKKSTIS 351

RESULT 2
Q9ZS03 PRELIMINARY: PRT: 351 AA.
AC Q9ZS03:
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE IM0UTANS (Hypothetical 40.6 kDa protein) (T10114.90)
DE (ATG422260/T10114.90).
GN IM.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN RP
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Wu D., Wright D.A., Weizel C., Voytas D.F., Rodermel S.R.;
RT "The IM0UTANS variegation locus of Arabidopsis defines a mitochondrial
RT alternative oxidase homologue that functions during early chloroplast
RT biogenesis."
RT Plant Cell 0:0-0(1999).
RN RN
RN SEQUENCE FROM N.A.
RA Liu S.X., Sakano H., Pham P.K., Yamada K., Banh J., Chung M.K.,
RA Toriumi M., Yu G., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Full length cDNA of gene T10114.90/ATG422260 (GI:7269072).";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN RN
RN SEQUENCE FROM N.A.
RA Shin P., Brooks S., Chao Q., Chen H., Kim C., Ecker J.;
RT "Full length cDNA sequences of Arabidopsis thaliana.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN RN
RN SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carrinci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shim P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene T10114.90/ATG422260 (GI:7269072).";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN RN
RN SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carrinci P., Dale J.M., Gibson H.A., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
RA Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
EMBL, AF098072; AAD03599.1; -

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DR EMBL: AF326898; AAC41480.1; -
DR EMBL: AF324663; AAC40014.1; -
DR EMBL: AF393717; AAK00399.1; -
DR EMBL: AY045699; AAK74057.1; -
DR InterPro: IPR002680; AOX.
DR Pfam: PF01786; AOX. 1.
KW Hypothetical protein.
SQ SEQUENCE 351 AA; 40574 MW; DBA38C9A4EC0EF69 CRC64;

Query Match 99.8%; Score 1841; DB 10; Length 351;
Best Local Similarity 99.7%; Pred. No. 2,2e-163;
Matches 350; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAISGISSTLTISRPLVTLRRSRAVSYSSSHRLHLPLSSRLLLRNNRQVATIL 60
Db 1 MAISGISSTLTISRPLVTLRRSRAVSYSSSHRLHLPLSSRLLLRNNRQVATIL 60
QY 61 ODDEKVVVEESFKAETSTGEPLLEPMMSSSTSAFEETWIKLEGVNFLTDSYKIL 120
Db 61 ODDEKVVVEESFKAETSTGEPLLEPMMSSSTSAFEETWIKLEGVNFLTDSYKIL 120
QY 121 DTLVDRRTYARFVLEETIARVYFAFMSVLMHMETFGMMRRADYLKVFHAESENEMHLL 180
Db 121 DTLVDRRTYARFVLEETIARVYFAFMSVLMHMETFGMMRRADYLKVFHAESENEMHLL 180
QY 181 IMEELGNSMWFDRFLAQHIAITFYMTVFLYLLSPMAVHSECVSHAETTYDKFLKA 240
Db 181 IMEELGNSMWFDRFLAQHIAITFYMTVFLYLLSPMAVHSECVSHAETTYDKFLKA 240
QY 241 SGEELKMPADIAVKYTGDLFLFDEPOTSRTPNTRRPVLENLADVNRDDAEHC 300
Db 241 SGEELKMPADIAVKYTGDLFLFDEPOTSRTPNTRRPVLENLADVNRDDAEHC 300
QY 301 KTRACQTLGSLRSPHSTLDDDDTEESGCVPEEAHCIGIVDCLKKSTIS 351
Db 301 KTRACQTLGSLRSPHSTLDDDDTEESGCVPEEAHCIGIVDCLKKSTIS 351

RESULT 3
Q949631 PRELIMINARY: PRT: 335 AA.
AC Q949631:
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE Hypothetical 38.7 kDa protein.
GN T10114.90 OR ATG422260.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN RN
RN SEQUENCE FROM N.A.
RA Bevan M., Murphy G., Drost L., Hall C., Hudson S., Ridley P.,
RA Bancroft I., Mewes H.W., Mayer K., Schell C.;
RT Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN RN
RN SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL021712; CAAL6776.1; -
DR EMBL: AL161557; CAB79181.1; -
DR InterPro: IPR002680; AOX.
DR Pfam: PF01786; AOX. 1.
KW Hypothetical protein.
SQ SEQUENCE 335 AA; 38674 MW; 3EE8063B73656B07 CRC64;

Query Match 94.3%; Score 1739; DB 10; Length 335;
Best Local Similarity 95.28; Pred. No. 6.8e-154;
Matches 334; Conservative 1; Mismatches 0; Indels 16; Gaps 1;
QY 1 MAISGISSTLTISRPLVTLRRSRAVSYSSSHRLHLPLSSRLLLRNNRQVATIL 60

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Db 1 MAALISGSSGTLTISRPLVLRRAAAYSSSSHRLHLPLSSRRLLRNHRVQATIL 60
Oy 61 ODDEKVVESFPAETSTGTEPLEEPNMSSSTSAFETWIKLEOGVNFLLTGSVIL 120
Db 61 ODDEKVVESFPAETSTGTEPLEEPNMSSSTSAFETWIKLEOGVNFLLTGSVIL 120
Oy 121 DTLVRDRTYARFFVLETTARVPYAFAMSVLHMVETFGWRRADYLKVFHFAESNMENHLL 180
Db 121 DTLVRDRTYARFFVLETTARVPYAFAMSVLHMVETFGWRRADYLKVFHFAESNMENHLL 180
Oy 181 IMBELGNSMWFDRFLAQHIAFTFYFMTVLYILSPRAYHFSCEVSHAYETDKELKA 240
Db 181 IMBELGNSMWFDRFLAQHIAFTFYFMTVLYILSPRAYHFSCEVSHAYETDKELKA 240
Oy 241 SGEELKNMPADIAVKYTGGLDLYLFDEFQTSRTNPRPVITENLYDFVNI RDDEAHC 300
Db 241 SGEELKNMPADIAVKYTGGLDLYLFDEFQTSRTNPRPVITENLYDFVNI RDDEAHC 300
Oy 301 KTRACQTLGSLRSPHSLTDDDTTEESGCVVPEAHCEGIVDCLKSI 351
Db 285 KTRACQTLGSLRSPHSLTDDDTTEESGCVVPEAHCEGIVDCLKSI 335

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RESULT 4

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OyFEC9 PRELIMINARY: PRT: 366 AA.
ID 09FEC9: 09FEC9: 09FEC9:
AC 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE Plastid quinol oxidase (Plastid terminal oxidase).
OS Lycopersicon esculentum (tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=CV. VENT CHERRY; TISSUE=LEAF;
RA Bae H., Behringer F., Wetzel C., Rodermel S.;
RT "IMMUTANS and GHOST are plastid quinol oxidases: evidence for a new
RT structural model of the mitochondrial alternative oxidase.";
RL submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN 12
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ATISA CRAIG; AND CV. RUTGER;
RC MEDLINE=20398337; PubMed=10938359;
RA Jose E.M., Simkin A.J., Gaffe J., Laboure A.M., Kuntz M., Carol P.;
RT "A Plastid Terminal Oxidase Associated with Carotenoid Desaturation
RT during Chromoplast Differentiation.";
RL Plant Physiol. 123:1427-1436(2000).
DR EMBL: AF302932; AAG18450.1; -
DR EMBL: AF177979; AAG02286.1; -
DR EMBL: AF177980; AAG02287.1; -
DR EMBL: AF302931; AAG18449.1; -
DR InterPro: IPR002680; AOX.
DR Pfam: PF01786; AOX. 1.
SQ SEQUENCE 366 AA: 41977 MM; 38C8D5141CCCA8FA CRC64;

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Query Match 66.7%; Score 1231; DB 10; Length 366;
 Best Local Similarity 66.3%; Pred. No. 1.9e-106;
 Matches 242; Conservative 40; Mismatches 57; Indels 26; Gaps 7;

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Oy 3 AATGSSGTLTISRPLVLRRAAAYSSSSHRLHLPLSSRRLLRNHRVQATIL 54
Db 4 S1SASFGTSVSSYSCFRARSEKSSVLCNSQNPFRNSVPIRKSQASCSVSRSKR 63
Oy 55 VQATLLODDEKVVESFPAETSTGTEPLEEPNMSSSTSAFETWIKLEO 106
Db 64 VQATLLODDEKVVESFPAETSTGTEPLEEPNMSSSTSAFETWIKLEO 117

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Oy 107 GAVNELTDSVYKILDFLYRDRTYARFFVLETTARVPYAFAMSVLHMVETFGWRRADYLK 166
Db 118 SVNILLTDSVYKILDFLYRDRTYARFFVLETTARVPYAFAMSVLHMVETFGWRRADYLK 177
Oy 167 VHFASNMENHLLIMBELGNSMWFDRFLAQHIAFTFYFMTVLYILSPRAYHFSCEV 226
Db 178 VHFASNMENHLLIMBELGNSMWFDRFLAQHIAFTFYFMTVLYILSPRAYHFSCEV 237
Oy 227 ESHAVETYDKFLKASGEELKNMPADIAVKYTGGLDLYLFDEFQTSRTNPRPVITENLY 286
Db 238 ESHAVETYDKFLKASGEELKNMPADIAVKYTGGLDLYLFDEFQTSRTNPRPVITENLY 297
Oy 287 DVEFVNI RDDEAHC KTRACQTLGSLRSPHSLTDDDTTEESGCVVPEAHCEGIVDCL 345
Db 298 DVEFVNI RDDEAHC KTRACQTLGSLRSPHSLTDDDTTEESGCVVPEAHCEGIVDCL 354
Oy 346 KKSIT 350
Db 355 KKSIT 359

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RESULT 5

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OyFEC9 PRELIMINARY: PRT: 357 AA.
ID 09FEC9: 09FEC9: 09FEC9:
AC 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE Plastid terminal oxidase.
OS Capsicum annuum (bell pepper).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxID=4072;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=CV. YOLO WONDER;
RC MEDLINE=20398337; PubMed=10938359;
RA Jose E.M., Simkin A.J., Gaffe J., Laboure A.M., Kuntz M., Carol P.;
RT "A Plastid Terminal Oxidase Associated with Carotenoid Desaturation
RT during Chromoplast Differentiation.";
RL Plant Physiol. 123:1427-1436(2000).
DR EMBL: AF177981; AAG02288.1; -
DR InterPro: IPR002680; AOX.
DR Pfam: PF01786; AOX. 1.
SQ SEQUENCE 357 AA: 41010 MM; 9047B0201A0CTD94 CRC64;

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Query Match 64.6%; Score 1191.5; DB 10; Length 357;
 Best Local Similarity 69.2%; Pred. No. 9.1e-103;
 Matches 227; Conservative 38; Mismatches 42; Indels 21; Gaps 5;

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Oy 29 SYSSSHLHLPLSSRRLLRNHRVQATILTDDDEKVVESFPAETSTGTEPLEEPNMSSST 81
Db 36 SLRNSHR-----TFQPSLSRKSRRVRAFLKENEDEVVERSFAPKSPGVNNGGNG 88
Oy 82 EPLEEPNMSSSTSAFETWIKLEOGVNFLLTGSVILKIDTLYRDRTYARFFVLETTARV 141
Db 89 EPPD-----NSSNGLEKWKVIKLEOGVNFLLTGSVILKIDTLYRDRTYARFFVLETTARV 143
Oy 142 PYAFAMSVLHMVETFGWRRADYLKVFHFAESNMENHLLIMBELGNSMWFDRFLAQHIA 201
Db 144 PYAFAMSVLHMVETFGWRRADYLKVFHFAESNMENHLLIMBELGNSMWFDRFLAQHIA 203
Oy 202 TFYFMTVLYILSPRAYHFSCEVSHAYETDKFLKASGEELKNMPADIAVKYTGGLD 261
Db 204 VFYFMTVLYILSPRAYHFSCEVSHAYETDKFLKASGEELKNMPADIAVKYTGGLD 263
Oy 262 DLYLFDEFQTSRTNPRPVITENLYDFVNI RDDEAHC KTRACQTLGSLRSPHSLTDD 321
Db 264 DLYLFDEFQTSRTNPRPVITENLYDFVNI RDDEAHC KTRACQTLGSLRSPHSLTDD 322
Oy 322 DTEESGCVVPEAHCEGIVDCLKSI 349

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Db 281 -----RLEPKDAKLDVTVTRADEAHN 302

RESULT 12

082807 PRELIMINARY; PRT; 332 AA.

AC 082807;

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Alternative oxidase.

GN AOX1A.

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Eubacteriales; Oryzae; Oryza.

OX NCBI_TaxID=4530;

RA [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. NTPRONBARE; TISSUE=CALLUS;

RA MEDLINE=98086211; PubMed=9426242;

RA Ito Y., Saito D., Nakazono M., Tsutsumi N., Hirai A.;

RT "Transcript levels of tandem-arranged alternative oxidase genes in rice are increased by low temperature.";

RL Gene 203:121-129(1997).

RL [2]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. HAYAYUKI; TISSUE=ANTHER;

RA Abe F., Kitashida H., Kishitani S., Toriyama K.;

RT "Isolation of a cDNA clone encoding the alternative oxidase expressed in rice anthers.";

RL Sex. plant Reprod. 10:374-375(1997).

DR EMBL; AB004864; BAA28773.1; -

DR EMBL; AB004813; BAA28772.1; -

DR EMBL; AB007452; BAA86963.1; -

DR InterPro; IPR002680; AOX.

DR Pfam; PF01786; AOX; 1.

SO SEQUENCE 332 AA; 37136 MW; 1A3C511404B60AD CRC64;

Query Match 10.8%; Score 199; DB 10; Length 332;

Best Local Similarity 27.5%; Pred. No. 3.3e-10;

Matches 73; Conservative 36; Mismatches 96; Indels 60; Gaps 10;

QY 62 DDEKVVV-----EESKATSTGTE-----PLEFPNSSSTSAFELWIKLEQV 108

Db 74 DAEKVVVNSWIGIOSSKLVREDGTETKMSCFRPM-----TYTADTSIDLTKHHV 125

QY 109 NVFLTDSV---IKIL---DTLYRDTYAFVLETIARYPYPAFMSVLHM---YET 155

Db 126 PKTLIDKIAVWTVKSRLRPDTIFQRRYGCAMMLETVAAPGVGGMILLSLRFRFQ 165

QY 156 FGMWRADYLVKVAESNEMHLLIMEELGNSWFDRELAQHTAFYFMVFLYILS 215

Db 186 SGGW-----ITLLEFAENEMHMLTMEV-ANPKWYERALVITVQGVFNAYFLGYLS 239

QY 216 PRMAYHSECVESHAYETDYELK-ASGEELKNMPAPDIAVKYTGDDLVLPDFQTSRT 274

Db 240 PKFAHRYVGYEEPAHSHYELKDLDAKIDNVPAALAIYW----- 283

QY 275 PNTRRPVLENLYDVFNIRDEDAH 299

Db 284 ---RLPANATLKDVTVVRADEAHN 305

RESULT 13

Q9LQ04 PRELIMINARY; PRT; 318 AA.

AC 09LQ04;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DE F5D14.11 protein.

GN F5D14.11.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RA [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. COLUMBIA;

RA Liu S.X., Chan A., Yu G., Lee J.M., Lenz C., Pham P., Sakano H.,

RA Toriumi M., Vysotskaya V.S., Chin C., Chou J., Choi E., Chung M.,

RA Gonzalez A., Howing B., Liu A., Vaysberg M., Altafi H., Brooks S.,

RA Buehler E., Chao Q., Conn L., Conway A.B., Hansen N.E.,

RA Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M., Nguyen M.,

RA Palm C.J., Shin P., Southwick A., Davis R.W., Ecker J.R.,

RA Fiedler N.A., Theologis A.;

RT "The sequence of BAC F5D14 from Arabidopsis thaliana chromosome 1.";

RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.

RL [2]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. COLUMBIA;

RA Theologis A.;

RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL; AC007767; AAF81331.1; -

DR InterPro; IPR002680; AOX.

DR Pfam; PF01786; AOX; 1.

SO SEQUENCE 318 AA; 36202 MW; F45F0526F86DD5A0 CRC64;

Query Match 10.5%; Score 194.5; DB 10; Length 318;

Best Local Similarity 25.9%; Pred. No. 8.3e-10;

Matches 83; Conservative 50; Mismatches 112; Indels 75; Gaps 17;

QY 16 RPLV--TLRRRAVSYSSHRLHLPLSRRL-----LRNNHVOATILQDDEK 66

Db 11 RPLVSSSVSSGGLGIGRFGH--LISHLP--NVRLLSPTSPVSGNNOPEPDIRAD-GK 66

QY 67 VYVEESFKAETSTGTEP--LEFPNSSSTSAFELW-----IKLEQV----- 109

Db 67 VI-----STWGIPTPTITTKPDGSAMKWCQFQWDSYKRPVSTIDVTKHHPNSFTK 119

QY 110 VFLTDSVIRKILDTLYRDTY-ARFVLETIARYPYPAFMSVLHM---YETFGWRRAD 163

Db 120 AVYTVQTLKIPQLPFRQRHMCAMMLETVAAPGVGGMILLSLRFRFSGW----- 175

QY 164 YLKVHVAESNEMHLLIMEELGNSWFD--FLAQHTAFYFMVFLYILSPRAY 220

Db 176 -IKALLEFAENEMHMLTPEIL-SQPKWYERAIPTVQGVFNAYFLA---YVISPKLAH 230

QY 221 HFECEVESHAYETDYELK-ASGEELKNMPAPDIAVKYTGDDLVLPDFQTSRTPR 279

Db 231 RTIGYILEEPAHVSYTEFLKDLDAKGFENSPALAIYW-----RL 271

QY 280 PVLENLYDVFNIRDEDAH 299

Db 272 PKDATLRDVVYVRADEAHN 291

RESULT 14

Q9AYP1 PRELIMINARY; PRT; 353 AA.

AC 09AYP1;

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)

DE Alternative oxidase.

OS Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; eucosids I; Gentianales; Apocynaceae; Rauvolfioideae;

OC Vincet; Catharanthus.

OX NCBI_TaxID=4058;

OX [1]

RP SEQUENCE FROM N.A.

RA Kiyota S., Sakano K.;
 RT "Catharantus roseus DNA for alternative oxidase."
 RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AB055060; BAB21500.1; -
 DR InterPro: IPR002680; AOX.
 DR Pfam: PF01786; AOX; 1.
 SQ SEQUENCE 353 AA: 40096 MW: 2BED4FCEDB65D00D CRC64;

Query Match 10.5%; Score 193; DB 10; Length 353;
 Best Local Similarity 23.5%; Pred. No. 1.3e-09;
 Matches 84; Conservative 53; Mismatches 124; Indels 96; Gaps 15;

QY 7 TGGGTTTSPVLTTRSSAAVSYSSRLHLHLPL-----SSRR- 46
 DB 2 MGRGATRISRLT---COISPRYFSSAAVRCHEPILGILTSGTTFPLHGNPGNGSERT 57
 QY 47 -----LLRNHHVQATLLODDEKVVESFKAETSTGEF-----LEPRMSS 92
 DB 58 ALTWIKLPMRRARSASTVATVDOKDEKREKNGVADGENSKAVSYWGVEAPRLKE 117
 QY 93 S-----TSAFETW-----IILKLGYNVFLTDSV-----IKIL-----DTLYRDRTYAR 131
 DB 118 DGTVMWTCGRPMETKRPDTEIELKHHVPVLLDKVAFTYKALRMPTDLFFQRTYGR 177
 QY 132 FVLELTIANVYVFAFNSVLH-----MYETFGMMRRADYLKHPAESWNEHLLIMEELG 186
 DB 178 AMLETVAAVPCGVWGMLHCKSLRFEHSGW-----IKALLEAEENERMHLMTFMEV- 231
 QY 187 GNSMWFDR---FLAOHIAFFYFMTVFLILSPRMAYHFSECVESHAYETFDKFLKASGE 243
 DB 232 SKRMTERLAFVGVGFNFNAYFLT--YLASPKLAHRIYGLYLEEPAIHSESEFLNEIDK 288
 QY 244 -ELKNMPADIAVKYTYGDLVLEDFQTSRTPNTRPIENLYDVFNIRDEDAH 299
 DB 289 GNENPAPALAIADYV-----QMPDSTLRDVMVYVRADEAH 326

RESULT 15
 Q8M4M4
 ID 08M4M4 PRELIMINARY: PRT: 326 AA.
 AC 08M4M4:
 DT 01-MAR-2002 (TREMblrel. 20, Created)
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Putative alternative oxidase.
 GN AOX.
 OS Vigna unguiculata (Cowpea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
 OX NCBI_TaxID=3917;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. EPAGE-1; TISSUE-LEAF;
 RA Costa J.H., Hasenratz-Sauder M.P., Jolivet Y., Fernandes de Melo D.,
 RA Pham-Thi A.T., Silva Lima M., Dizengremel P.;
 RT "Identification and sequencing of two cDNA clones encoding Vigna
 RT unguiculata alternative oxidase."
 RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AJ421015; CAD12835.1; -
 DR InterPro: IPR002680; AOX.
 DR Pfam: PF01786; AOX; 1.
 SQ SEQUENCE 326 AA: 37247 MW: C6268A871E8B8400 CRC64;

Query Match 10.4%; Score 192; DB 10; Length 326;
 Best Local Similarity 25.8%; Pred. No. 1.5e-09;
 Matches 85; Conservative 41; Mismatches 121; Indels 82; Gaps 14;

QY 20 TLRSSRAAVSYSSRLHLHLPLSS-----RL-----LLRNNHRYO 56
 DB 4 TLVRSAAARLLGGGRYRHAFTPAIVETRGHGGAGFSLKRNSTLPDIKDNSEK 63
 QY 57 ATLQDDEKVVESF-----KAETSTGTETLEPNNMSSSTSAFETW-----IILK 103

DB 64 KNEYDDMTNNAVSISSYWGISRPKVAREDEGT-----WPNMCFPMWDTYHSDVSI 114
 QY 104 LEQGNVFLTDSV-----IKILDLY-RDRYARFVLETIARVYFAFMSVLHMYET 155
 DB 115 TKHHTPKSLTRKVAFRSVKFLRVLSDLVFKERYCHAMMETIAYVGMVGMGLHLKSL 174
 QY 156 FGMMRRADYLKHPAESWNEHLLIMEELGNSMWFDR---FLAOHIAFFYFMTVFLY 212
 DB 175 RKFGSGGMITALLLEAEENERMHLMTVYL-VQPKHIERLLIFTAOGV--FFNAFVY-Y 230
 QY 213 ILSPRMAYHFSECVESHAYETFDKFLKA--SGEELKNMPADIAVKYTYGDLVLPDEFQ 270
 DB 231 LLSPKAAHFRVGYLLEEAIVISTQHLLEAFESG-KVENVPAPALAIADYV----- 277
 QY 271 TSRTPNTRPIENLYDVFNIRDEDAH 299
 DB 278 -----RLPKDATILKDVVTVVIRADEAH 299

Search completed: February 2, 2003, 22:47:49
 Job time : 89 secs

